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                    GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:       September 13, 2004, 12:16:04 ; Search time 130 Seconds
                                    (without alignments)
                                    490.902 Million cell updates/sec

Title:        US-10-735-594-1
Perfect score: 1043
Sequence:     1 LPICPGGAARCQVTLRDLFD.........HKIDNYLKLLKCRIIHNNNC 199

Scoring table: BLOSUM62
              Gapop 10.0 , Gapext 0.5

Searched:     1335176 seqs, 320689617 residues

Total number of hits satisfying chosen parameters:    1335176

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :    Published Applications AA:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1043	100.0	199	14	US-10-153-207-4	Sequence 4, Appli
2	1043	100.0	200	10	US-09-819-094-9	Sequence 9, Appli
3	1043	100.0	200	16	US-10-714-067-9	Sequence 9, Appli
4	1043	100.0	227	9	US-09-815-305-1	Sequence 1, Appli
5	1043	100.0	227	12	US-10-221-278-226	Sequence 226, App
6	1043	100.0	227	14	US-10-140-293-3	Sequence 3, Appli
7	1043	100.0	227	15	US-10-291-172-226	Sequence 226, App
8	1039	99.6	228	12	US-09-065-330D-2	Sequence 2, Appli
9	1035	99.2	200	16	US-10-449-609-1	Sequence 1, Appli
10	1035	99.2	227	14	US-10-140-293-4	Sequence 4, Appli
11	1035	99.2	385	16	US-10-449-609-6	Sequence 6, Appli
12	1031	98.8	199	14	US-10-449-609-12	Sequence 12, Appli
13	1026.5	98.4	579	16	US-10-449-609-7	Sequence 7, Appli
14	1026.5	98.4	942	16	US-10-449-609-8	Sequence 8, Appli
15	895	85.8	199	14	US-10-140-293-24	Sequence 24, Appl
16	887	85.0	199	14	US-10-140-293-21	Sequence 21, Appl
17	881	84.5	199	14	US-10-140-293-22	Sequence 22, Appl
18	865	82.9	199	14	US-10-140-293-16	Sequence 16, Appl
19	863.5	82.8	198	14	US-10-140-293-30	Sequence 30, Appl
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22	782	75.0	199	14	US-10-140-293-19	Sequence 19, Appl
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24	775	74.3	199	14	US-10-140-293-29	Sequence 29, Appl
25	772	74.0	199	14	US-10-140-293-17	Sequence 17, Appl
26	760	72.9	210	12	US-10-424-599-276669	Sequence 276669,
27	748	71.7	199	14	US-10-140-293-25	Sequence 25, Appl
28	747	71.6	199	14	US-10-140-293-26	Sequence 26, Appl
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31	725.5	69.6	258	12	US-10-221-278-602	Sequence 602, App
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33	705	67.6	140	10	US-09-819-094-11	Sequence 11, Appl
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39	663	63.6	197	14	US-10-140-293-13	Sequence 13, Appl
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41	630	60.4	125	13	US-10-036-869-25	Sequence 25, Appl
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44	626	60.0	124	16	US-10-714-067-10	Sequence 10, Appl
45	612	58.7	197	14	US-10-140-293-14	Sequence 14, Appl

ALIGNMENTS

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RESULT 1
US-10-153-207-4
; Sequence 4, Application US/1015207
; Publication No. US2003015003A1
; GENERAL INFORMATION:
;  APPLICANT: James A. Wells
;  APPLICANT: Brian C. Cunningham
;  TITLE OF INVENTION: GROWTH HORMONE VARIANTS
;  FILE REFERENCE: 669.12-US-C7
;  CURRENT APPLICATION NUMBER: US/10/153,207
;  CURRENT FILING DATE:  2002-05-22
;  PRIOR APPLICATION NUMBER: 08/479,884
;  PRIOR FILING DATE: 1995-06-07
;  PRIOR APPLICATION NUMBER: 08/190,723
;  PRIOR FILING DATE: 1994-02-02
;  PRIOR APPLICATION NUMBER: 07/960,227
;  PRIOR FILING DATE: 1992-10-13
;  PRIOR APPLICATION NUMBER: 07/875,204
;  PRIOR FILING DATE: 1992-04-27
;  PRIOR APPLICATION NUMBER: 07/428,066
;  PRIOR FILING DATE: 1989-10-26
;  PRIOR APPLICATION NUMBER: 07/264,611
;  PRIOR FILING DATE: 1988-10-28
;  NUMBER OF SEQ ID NOS: 20
;  SOFTWARE: FastSEQ for Windows Version 4.0
;  SEQ ID NO 4
;    LENGTH: 199
;    TYPE: PRT
;    ORGANISM: Homo Sapiens
US-10-153-207-4

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Best Local Similarity 100.0%;  Pred. No. 1.6e-101;
Matches 199;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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US-09-819-094-9
; Sequence 9, Application US/09819094
; Publication No. US2003018638A1
; GENERAL INFORMATION:
;   APPLICANT: Weiner, Richard I.
;   APPLICANT: Martial, Joseph A.
;   APPLICANT: Struman, Ingrid
;   APPLICANT: Taylor, Robert
;   APPLICANT: Bentzien, Frauke
;   TITLE OF INVENTION: No. US2003018638A2le1 Antiangiogenic Peptide Agents and Their
;   TITLE OF INVENTION: Therapeutic and Diagnostic Use
;   FILE REFERENCE: UCSF-018/02US
;   CURRENT APPLICATION NUMBER: US/09/819,094
;   CURRENT FILING DATE: 2001-03-27
;   PRIOR APPLICATION NUMBER: 09/076,675
;   PRIOR FILING DATE: 1998-05-12
;   PRIOR APPLICATION NUMBER: 60/046,394
;   PRIOR FILING DATE: 1997-05-12
;   NUMBER OF SEQ ID NOS: 34
; SEQ ID NO 9
;   LENGTH: 200
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-819-094-9

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RESULT 3
US-10-714-067-9
; Sequence 9, Application US/10714067
; Publication No. US2004007705A1
; GENERAL INFORMATION:
;   APPLICANT: Weiner, Richard I.
;   APPLICANT: Martial, Joseph A.
;   APPLICANT: Struman, Ingrid
;   APPLICANT: Taylor, Robert
;   APPLICANT: Bentzien, Frauke
;   TITLE OF INVENTION: Novel Antiangiogenic Peptide Agents and Their
;   TITLE OF INVENTION: Therapeutic and Diagnostic Use
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;   FILE REFERENCE: UCSF-018/02US
;   CURRENT APPLICATION NUMBER: US/10/714,067
;   CURRENT FILING DATE: 2003-11-14
;   PRIOR APPLICATION NUMBER: US/09/819,094
;   PRIOR FILING DATE: 2001-03-27
;   PRIOR APPLICATION NUMBER: 09/076,675
;   PRIOR FILING DATE: 1998-05-12
;   PRIOR APPLICATION NUMBER: 60/046,394
;   PRIOR FILING DATE: 1997-05-12
;   NUMBER OF SEQ ID NOS: 34
; SEQ ID NO 9
;   LENGTH: 200
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-10-714-067-9

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US-09-815-306-1
; Sequence 1, Application US2020068043A1
; Patent No. US20020068043A1
; GENERAL INFORMATION:
;   APPLICANT: WAGNER, THOMAS E.
;   APPLICANT: CHEN, WEN Y.
;   TITLE OF INVENTION: BI-FUNCTIONAL CANCER TREATMENT AGENTS
;   FILE REFERENCE: 035879/0120
;   CURRENT APPLICATION NUMBER: US/09/815,306
;   CURRENT FILING DATE: 2001-03-23
;   PRIOR APPLICATION NUMBER: 60/191,457
;   PRIOR FILING DATE: 2000-03-23
;   NUMBER OF SEQ ID NOS: 33
;   SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
;   LENGTH: 227
;   TYPE: PRT
;   ORGANISM: Homo sapiens
US-09-815-306-1

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; Sequence 226, Application US/10221278
; Publication No. US20040034208A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc
;  TITLE OF INVENTION: No. US20040034208A1e1 Nucleic Acids and Polypeptides
;  FILE REFERENCE: 21272-045
;  CURRENT APPLICATION NUMBER: US/10/221,278
;  CURRENT FILING DATE: 2002-09-06
;  PRIOR APPLICATION NUMBER: 09/693,267
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 09/665,363
;  PRIOR FILING DATE: 2000-09-19
;  PRIOR APPLICATION NUMBER: 09/616,847
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: 09/596,193
;  PRIOR FILING DATE: 2000-06-17
;  PRIOR APPLICATION NUMBER: 09/574,454
;  PRIOR FILING DATE: 2000-05-19
;  PRIOR APPLICATION NUMBER: 09/519,705
;  PRIOR FILING DATE: 2000-03-07
;  NUMBER OF SEQ ID NOS: 752
;  SEQ ID NO 226
;  LENGTH: 227
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-10-221-278-226

Query Match           100.0%;  Score 1043;  DB 12;  Length 227;
Best Local Similarity 100.0%;  Pred. No. 1.9e-101;
Matches 199;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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RESULT 6
US-10-140-293-3
; Sequence 3, Application US/10140293
; Publication No. US20030022833A1
; GENERAL INFORMATION:
;  APPLICANT: CHEN, WEN Y.
;  APPLICANT: WAGNER, THOMAS E.
;  TITLE OF INVENTION: USE OF ANTI-PROLACTIN AGENTS TO TREAT PORLIFERATIVE
;  TITLE OF INVENTION: CONDITIONS
;  FILE REFERENCE: 035879/0109
;  CURRENT APPLICATION NUMBER: US/10/140,293
;  CURRENT FILING DATE: 2002-05-08
;  PRIOR APPLICATION NUMBER: US/09/246,041
;  PRIOR FILING DATE: 1999-02-05
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.1
;  SEQ ID NO 3
;  LENGTH: 227
;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-10-140-293-3

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Best Local Similarity 100.0%;  Pred. No. 1.9e-101;
Matches 199;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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Qy   181 KIDNYLKLLKCRIIHNNNC 199
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RESULT 7
US-10-291-172-226
; Sequence 226, Application US/10291172
; Publication No. US2003022858A1
; GENERAL INFORMATION:
;  APPLICANT: Hyseq, Inc
;  TITLE OF INVENTION: No. US20030228584A1e1 Nucleic Acids and Polypeptides
;  FILE REFERENCE: 21272-045
;  CURRENT APPLICATION NUMBER: US/10/291,172
;  CURRENT FILING DATE: 2000-11-08
;  PRIOR APPLICATION NUMBER: 09/693,267
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 09/665,363
;  PRIOR FILING DATE: 2000-09-19
;  PRIOR APPLICATION NUMBER: 09/616,847
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: 09/596,193
;  PRIOR FILING DATE: 2000-06-17
;  PRIOR APPLICATION NUMBER: 09/574,454
;  PRIOR FILING DATE: 2000-05-19
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;  PRIOR FILING DATE: 2000-03-07
;  NUMBER OF SEQ ID NOS: 752
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;  TYPE: PRT
;  ORGANISM: Homo sapiens
US-10-291-172-226

Query Match           100.0%;  Score 1043;  DB 15;  Length 227;
Best Local Similarity 100.0%;  Pred. No. 1.9e-101;
Matches 199;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

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RESULT 8
US-09-065-330D-2
; Sequence 2, Application US/09065330D
; Publication No. US2001003662A1
; GENERAL INFORMATION:
; APPLICANT: WALKER, Ameae M.
; TITLE OF INVENTION: PROLACTIN ANTAGONISTS AND USES THEREOF
; FILE REFERENCE: 39754-0611-1CP1CP
; CURRENT APPLICATION NUMBER: US/09/065,330D
; CURRENT FILING DATE: 1998-04-23
; PRIOR APPLICATION NUMBER: PCT/US97/01435
; PRIOR FILING DATE: 1997-01-30
; PRIOR APPLICATION NUMBER: US 08/594,809
; PRIOR FILING DATE: 1996-01-31
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSBQ for Windows Version 4.0
; SEQ ID NO 2
; LENGTH: 228
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: VARIANT
; LOCATION: 208
; OTHER INFORMATION: Site mutated amino acid residue where the normal
; OTHER INFORMATION: codon coding for serine is modified preferably to encode
; OTHER INFORMATION: for aspartate or glutamate, most preferably
; OTHER INFORMATION: aspartate.
US-09-065-330D-2

  Query Match       99.6%;    Score 1039;  DB 12;  Length 228;
  Best Local Similarity  99.5%;  Pred. No. 5.1e-101;
  Matches  198;  Conservative  0;  Mismatches  0;  Indels  1;  Gaps  0;

Qy    1 LPICPGGAARCQVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFITKAINSCHT 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   30 LPICPGGAARCQVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFITKAINSCHT 89

Qy   61 SSLATPEDKEQAQQMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   90 SSLATPEDKEQAQQMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 149

Qy  121 EQTKRLLEGMELIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSH 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  150 EQTKRLLEGMELIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSH 209

Qy  181 KIDNYLKLLKCRIIHNNNC 199
        |||||||||||||||||||
Db  210 KIDNYLKLLKCRIIHNNNC 228

RESULT 9
US-10-449-609-1
; Sequence 1, Application US/10449609
; Publication No. US20040127407A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, WEN Y
; TITLE OF INVENTION: HUMAN PROLACTIN ANTAGONIST-ANGIOGENESIS INHIBITOR
; TITLE OF INVENTION: FUSION PROTEINS
; FILE REFERENCE: 035879-0163
; CURRENT APPLICATION NUMBER: US/10/449,609
; CURRENT FILING DATE: 2003-09-26
; PRIOR APPLICATION NUMBER: 60/384,121
; PRIOR FILING DATE: 2002-05-31
; NUMBER OF SEQ ID NOS: 45
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 200
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-449-609-1
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  Query Match       99.2%;    Score 1035;  DB 16;  Length 200;
  Best Local Similarity  99.5%;  Pred. No. 1.1e-100;
  Matches  198;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy    1 LPICPGGAARCQVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFITKAINSCHT 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    2 LPICPGGAARCQVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFITKAINSCHT 61

Qy   61 SSLATPEDKEQAQQMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   62 SSLATPEDKEQAQQMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 121

Qy  121 EQTKRLLEGMELIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSH 180
        ||||||||||||||||||||||||||||||||||||| ||||||||||||||||||||||
Db  122 EQTKRLLERMELIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSH 181

Qy  181 KIDNYLKLLKCRIIHNNNC 199
        |||||||||||||||||||
Db  182 KIDNYLKLLKCRIIHNNNC 200

RESULT 10
US-10-140-293-4
; Sequence 4, Application US/10140293
; Publication No. US20030022833A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, WEN Y.
; APPLICANT: WAGNER, THOMAS E.
; TITLE OF INVENTION: USE OF ANTI-PROLACTIN AGENTS TO TREAT PORLIFERATIVE
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 035879/0109
; CURRENT APPLICATION NUMBER: US/10/140,293
; CURRENT FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US/09/246,041
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 4
; LENGTH: 227
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-140-293-4

  Query Match       99.2%;    Score 1035;  DB 14;  Length 227;
  Best Local Similarity  99.5%;  Pred. No. 1.3e-100;
  Matches  198;  Conservative  0;  Mismatches  1;  Indels  0;  Gaps  0;

Qy    1 LPICPGGAARCQVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFITKAINSCHT 60
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Db   29 LPICPGGAARCQVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFITKAINSCHT 88

Qy   61 SSLATPEDKEQAQQMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 120
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   89 SSLATPEDKEQAQQMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 148

Qy  121 EQTKRLLEGMELIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSH 180
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  149 EQTKRLLEGMELIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSH 208

Qy  181 KIDNYLKLLKCRIIHNNNC 199
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Db  209 KIDNYLKLLKCRIIHNNNC 227

RESULT 11
US-10-449-609-6
; Sequence 6, Application US/10449609
; Publication No. US20040127407A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, WEN Y
; TITLE OF INVENTION: HUMAN PROLACTIN ANTAGONIST-ANGIOGENESIS INHIBITOR
; TITLE OF INVENTION: FUSION PROTEINS
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;      FILE REFERENCE: 035879-0163
;      CURRENT APPLICATION NUMBER: US/10/449,609
;      CURRENT FILING DATE: 2003-09-26
;      PRIOR APPLICATION NUMBER: 60/384,121
;      PRIOR FILING DATE: 2002-05-31
;      NUMBER OF SEQ ID NOS: 45
;      SOFTWARE: PatentIn Ver. 2.1
;   SEQ ID NO 6
;      LENGTH: 385
;      TYPE: PRT
;      ORGANISM: Artificial Sequence
;      FEATURE:
;      OTHER INFORMATION: Description of Artificial Sequence: Fusion protein
US-10-449-609-6

Query Match             99.2%;  Score 1035;  DB 16;  Length 385;
Best Local Similarity   99.5%;  Pred. No. 2.8e-100;
  Matches  198;  Conservative    0;  Mismatches    1;  Indels    0;  Gaps    0;

Qy          1 LPICPGGAARCQVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFITKAINSCHT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          2 LPICPGGAARCQVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFITKAINSCHT 61

Qy         61 SSLATPEDKEQAQQMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         62 SSLATPEDKEQAQQMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 121

Qy        121 EQTKRLLEGMELIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSH 180
              ||||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db        122 EQTKRLLERMELIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSH 181

Qy        181 KIDNYLKLLKCRIIHNNNC 199
              |||||||||||||||||||
Db        182 KIDNYLKLLKCRIIHNNNC 200

RESULT 12
US-10-140-293-12
;   Sequence 12, Application US/10140293
;   Publication No. US20030022833A1
;   GENERAL INFORMATION:
;      APPLICANT: CHEN, WEN Y.
;      APPLICANT: WAGNER, THOMAS E.
;      TITLE OF INVENTION: USE OF ANTI-PROLACTIN AGENTS TO TREAT PORLIFERATIVE
;      TITLE OF INVENTION: CONDITIONS
;      FILE REFERENCE: 035879/0109
;      CURRENT APPLICATION NUMBER: US/10/140,293
;      CURRENT FILING DATE: 2002-05-08
;      PRIOR APPLICATION NUMBER: US/09/246,041
;      PRIOR FILING DATE: 1999-02-05
;      NUMBER OF SEQ ID NOS: 42
;      SOFTWARE: PatentIn Ver. 2.1
;   SEQ ID NO 12
;      LENGTH: 199
;      TYPE: PRT
;      ORGANISM: Homo sapiens
US-10-140-293-12

Query Match             98.8%;  Score 1031;  DB 14;  Length 199;
Best Local Similarity   98.5%;  Pred. No. 2.9e-100;
  Matches  196;  Conservative    1;  Mismatches    2;  Indels    0;  Gaps    0;

Qy          1 LPICPGGAARCQVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFITKAINSCHT 60
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db          1 LPICPGGAARCQVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFITKAINSCHT 60

Qy         61 SSLATPEDKEQAQQMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SSLATPEDKEQAQQMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 120

Qy        121 EQTKRLLEGMELIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSH 180
              |||||||:|||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EQTKRLLRGMELIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSH 180
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Qy        181 KIDNYLKLLKCRIIHNNNC 199
              |||||||||||||||||||
Db        181 KIDNYLKLLKCRIIHNNNC 199

RESULT 13
US-10-449-609-7
;   Sequence 7, Application US/10449609
;   Publication No. US20040127407A1
;   GENERAL INFORMATION:
;      APPLICANT: CHEN, WEN Y
;      TITLE OF INVENTION: HUMAN PROLACTIN ANTAGONIST-ANGIOGENESIS INHIBITOR
;      TITLE OF INVENTION: FUSION PROTEINS
;      FILE REFERENCE: 035879-0163
;      CURRENT APPLICATION NUMBER: US/10/449,609
;      CURRENT FILING DATE: 2003-09-26
;      PRIOR APPLICATION NUMBER: 60/384,121
;      PRIOR FILING DATE: 2002-05-31
;      NUMBER OF SEQ ID NOS: 45
;      SOFTWARE: PatentIn Ver. 2.1
;   SEQ ID NO 7
;      LENGTH: 579
;      TYPE: PRT
;      ORGANISM: Artificial Sequence
;      FEATURE:
;      OTHER INFORMATION: Description of Artificial Sequence: Fusion protein
US-10-449-609-7

Query Match             98.4%;  Score 1026.5;  DB 16;  Length 579;
Best Local Similarity   99.5%;  Pred. No. 4e-99;
  Matches  198;  Conservative    0;  Mismatches    0;  Indels    1;  Gaps    1;

Qy          1 LPICPGGAARCQVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFITKAINSCHT 60
              |||||||||||||||||||||||||||||||||||||||||||||||| |||||||||||
Db          2 LPICPGGAARCQVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGR-FITKAINSCHT 60

Qy         61 SSLATPEDKEQAQQMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 120
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db         61 SSLATPEDKEQAQQMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 120

Qy        121 EQTKRLLEGMELIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSH 180
              ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db        121 EQTKRLLEGMELIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSH 180

Qy        181 KIDNYLKLLKCRIIHNNNC 199
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Db        181 KIDNYLKLLKCRIIHNNNC 199

RESULT 14
US-10-449-609-8
;   Sequence 8, Application US/10449609
;   Publication No. US20040127407A1
;   GENERAL INFORMATION:
;      APPLICANT: CHEN, WEN Y
;      TITLE OF INVENTION: HUMAN PROLACTIN ANTAGONIST-ANGIOGENESIS INHIBITOR
;      TITLE OF INVENTION: FUSION PROTEINS
;      FILE REFERENCE: 035879-0163
;      CURRENT APPLICATION NUMBER: US/10/449,609
;      CURRENT FILING DATE: 2003-09-26
;      PRIOR APPLICATION NUMBER: 60/384,121
;      PRIOR FILING DATE: 2002-05-31
;      NUMBER OF SEQ ID NOS: 45
;      SOFTWARE: PatentIn Ver. 2.1
;   SEQ ID NO 8
;      LENGTH: 942
;      TYPE: PRT
;      ORGANISM: Artificial Sequence
;      FEATURE:
;      OTHER INFORMATION: Description of Artificial Sequence: Fusion protein
US-10-449-609-8
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Wed Sep 15 08:30:10 2004

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Query Match        98.4%;   Score 1026.5;  DB 16;  Length 942;
Best Local Similarity  99.5%;   Pred. No. 8e-99;
Matches  198;  Conservative  0;  Mismatches  0;  Indels  1;  Gaps  1;

Qy    1 LPICPGGAARCQVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFITKAINSCHT 60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||| ||||||||
Db    2 LPICPGGAARCQVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGR-FITKAINSCHT 60

Qy   61 SSLATPEDKEQAQQMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   61 SSLATPEDKEQAQQMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 120

Qy  121 EQTKRLLEGMELIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSH 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  121 EQTKRLLEGMELIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSH 180

Qy  181 KIDNYLKLLKCRIIHNNNC 199
        |||||||||||||||||||
Db  181 KIDNYLKLLKCRIIHNNNC 199


RESULT 15
US-10-140-293-24
; Sequence 24, Application US/10140293
; Publication No. US20030022833A1
; GENERAL INFORMATION:
;  APPLICANT: CHEN, WEN Y.
;  APPLICANT: WAGNER, THOMAS E.
;  TITLE OF INVENTION: USE OF ANTI-PROLACTIN AGENTS TO TREAT PORLIFERATIVE
;  TITLE OF INVENTION: CONDITIONS
;  FILE REFERENCE: 035879/0109
;  CURRENT APPLICATION NUMBER: US/10/140,293
;  CURRENT FILING DATE: 2002-05-08
;  PRIOR APPLICATION NUMBER: US/09/246,041
;  PRIOR FILING DATE: 1999-02-05
;  NUMBER OF SEQ ID NOS: 42
;  SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 24
;  LENGTH: 199
;  TYPE: PRT
;  ORGANISM: Unknown Sequence
;  FEATURE:
;  OTHER INFORMATION: Description of Artificial Sequence: Ancestral mammal
US-10-140-293-24

Query Match        85.8%;   Score 895;  DB 14;  Length 199;
Best Local Similarity  83.4%;   Pred. No. 6.5e-86;
Matches  166;  Conservative  17;  Mismatches  16;  Indels  0;  Gaps  0;

Qy    1 LPICPGGAARCQVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFITKAINSCHT 60
        ||||| ||:|||||||||:|||||||||||||||||||||:||||||: |||||||||||||
Db    1 LPICPSGAVNCQVSLRDLFDRAVILSHYIHNLSSEMFNEFDKRYAQGRGFITKAINSCHT 60

Qy   61 SSLATPEDKEQAQQMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 120
        ||||||||||||:::::::|||:::: |:||:|||||||||||||||||||||:|||:||||
Db   61 SSLSTPEDKEQAQQIHHEVLLNLILGLLRSWNDPLYHLVTEVRGMQEAPEAILSRAIEIE 120

Qy  121 EQTKRLLEGMELIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSH 180
        |::|||||||:||::||||| ||||| ||||||||||||||::|||:|:|||||||||||||
Db  121 EENKRLLEGMEKIVGQVHPGAKENEIYSVWSGLPSLQMADEDSRLFAFYNLLHCLRRDSH 180

Qy  181 KIDNYLKLLKCRIIHNNNC 199
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Db  181 KIDNYLKLLKCRIIYNNNC 199
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Search completed: September 13, 2004, 12:27:43
Job time : 131 secs

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          GenCore version 5.1.6
     Copyright (c) 1993 - 2004 Compugen Ltd.
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OM protein - protein search, using sw model

Run on: September 13, 2004, 11:37:20 ; Search time 123 Seconds
                                           (without alignments)
                           457.130 Million cell updates/sec

Title: US-10-735-594-1
Perfect score: 1043
Sequence: 1 LPICPGGAARCQVTLRDLFD.........HKIDNYLKLLKCRIIHNNNC 199

Scoring table: BLOSUM62
              Gapop 10.0 , Gapext 0.5
Searched: 1586107 seqs, 282547505 residues

Total number of hits satisfying chosen parameters: 1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database : A_Geneseq_29jan04:*
         1: geneseqp1980s:*
         2: geneseqp1990s:*
         3: geneseqp2000s:*
         4: geneseqp2001s:*
         5: geneseqp2002s:*
         6: geneseqp2003as:*
         7: geneseqp2003bs:*
         8: geneseqp2004s:*
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SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

| Result No. | Score | % Query Match | Length | DB | ID | Description |
|---|---|---|---|---|---|---|
| 1 | 1043 | 100.0 | 199 | 2 | AAY31764 | Aay31764 Human pro |
| 2 | 1043 | 100.0 | 199 | 5 | ABG94847 | Abg94847 Human pro |
| 3 | 1043 | 100.0 | 200 | 2 | AAW92258 | Aaw92258 Human ant |
| 4 | 1043 | 100.0 | 227 | 2 | AAR05231 | Aar05231 AA sequen |
| 5 | 1043 | 100.0 | 227 | 4 | AAG78336 | Aag78336 Human pro |
| 6 | 1043 | 100.0 | 227 | 6 | AAU28057 | Aau28057 Novel hum |
| 7 | 1043 | 100.0 | 227 | 7 | ADD48810 | Add48810 Human Pro |
| 8 | 1043 | 100.0 | 351 | 2 | AAR78691 | Aar78691 Prolactin |
| 9 | 1039 | 99.6 | 228 | 2 | AAW23626 | Aaw23626 Prolactin |
| 10 | 1039 | 99.6 | 228 | 2 | AAW23620 | Aaw23620 Prolactin |
| 11 | 1038 | 99.5 | 199 | 3 | AAY78428 | Aay78428 Human pro |
| 12 | 1036 | 99.3 | 199 | 2 | ABU09846 | Abu09846 Human pro |
| 13 | 1036 | 99.3 | 359 | 2 | AAR05805 | Aar05805 DHFR-prol |
| 14 | 1035 | 99.2 | 227 | 4 | AAG78337 | Aag78337 Mutant hu |
| 15 | 1034 | 99.1 | 227 | 1 | AAP82079 | Aap82079 Human pre |
| 16 | 1028 | 98.6 | 199 | 6 | ABU09878 | Abu09878 Human pro |
| 17 | 1022 | 98.0 | 199 | 2 | AAW23629 | Aaw23629 Human pro |
| 18 | 895 | 85.8 | 199 | 6 | ABU09858 | Abu09858 Ancestral |
| 19 | 881 | 84.5 | 199 | 6 | ABU09856 | Abu09856 Horse pro |
| 20 | 877 | 84.1 | 199 | 6 | ABU09855 | Abu09855 Camel pro |
| 21 | 873 | 83.7 | 199 | 6 | ABU09864 | Abu09864 Ancestral |
| 22 | 866 | 83.0 | 199 | 6 | ABU09854 | Abu09854 Pig prola |
| 23 | 865 | 82.9 | 199 | 6 | ABU09850 | Abu09850 Finback w |
| 24 | 794 | 76.1 | 240 | 6 | ABR43658 | Abr43658 Ovine pro |
| 25 | 792 | 75.9 | 199 | 6 | ABU09852 | Abu09852 Cow prola |
| 26 | 791.5 | 75.9 | 198 | 6 | ABU09861 | Abu09861 Sea turtl |
| 27 | 782 | 75.0 | 199 | 6 | ABU09853 | Abu09853 Sheep pro |
| 28 | 776 | 74.4 | 199 | 6 | ABU09862 | Abu09862 Crocodile |
| 29 | 775 | 74.3 | 199 | 6 | ABU09863 | Abu09863 Alligator |
| 30 | 772 | 74.0 | 199 | 6 | ABU09851 | Abu09851 Mink prol |
| 31 | 754 | 72.3 | 199 | 2 | AAR87090 | Aar87090 Turkey pr |
| 32 | 754 | 72.3 | 426 | 2 | AAR87091 | Aar87091 Turkey pr |
| 33 | 748 | 71.7 | 199 | 6 | ABU09859 | Abu09859 Chicken p |
| 34 | 748 | 71.7 | 229 | 6 | AAR05699 | Aar05699 Preprolac |
| 35 | 747 | 71.6 | 199 | 6 | ABU09860 | Abu09860 Turkey pr |
| 36 | 737 | 70.7 | 199 | 6 | ABU09857 | Abu09857 Asiatic e |
| 37 | 725.5 | 69.6 | 258 | 4 | AAU28245 | Aau28245 Novel hum |
| 38 | 710 | 68.1 | 167 | 6 | AAO16658 | Aao16658 Human ext |
| 39 | 705 | 67.6 | 140 | 2 | AAW92260 | Aaw92260 Human ant |
| 40 | 705 | 67.6 | 143 | 2 | AAW92261 | Aaw92261 Human ant |
| 41 | 697 | 66.8 | 173 | 6 | AAO16662 | Aao16662 Human ext |
| 42 | 696 | 66.7 | 199 | 6 | ABU09865 | Abu09865 Clawed fr |
| 43 | 690.5 | 66.2 | 199 | 6 | ABU09866 | Abu09866 Bullfrog |
| 44 | 689.5 | 66.1 | 184 | 1 | AAP70504 | Aap70504 Cattle re |
| 45 | 667 | 64.0 | 226 | 2 | AAR14599 | Aar14599 Rat prola |

ALIGNMENTS

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ID   AAY31764 standard; protein; 199 AA.
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AC   AAY31764;
XX
DT   06-DEC-1999  (first entry)
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DE   Human prolactin.
XX
KW   Prolactin; human; variant; protein engineering.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
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FT                   /note= "optionally substituted by Phe in human prolactin
FT                   variant of Claim 8"
FT   Misc-difference 60
FT                   /note= "optionally substituted by Ser in human prolactin
FT                   variant of Claim 8"
FT   Misc-difference 61
FT                   /note= "optionally substituted by Glu in human prolactin
FT                   variant of Claim 8"
FT   Misc-difference 63
FT                   /note= "optionally substituted by Ile in human prolactin
FT                   variant of Claim 8"
FT   Misc-difference 64
FT                   /note= "optionally substituted by Pro in human prolactin
FT                   variant of Claim 8"
FT   Misc-difference 67
FT                   /note= "optionally substituted by Ser in human prolactin
FT                   variant of Claim 8"
FT   Misc-difference 68
FT                   /note= "optionally substituted by Asn in human prolactin
FT                   variant of Claim 8"
FT   Misc-difference 69
FT                   /note= "optionally substituted by Arg in human prolactin
FT                   variant of Claim 8"
FT   Misc-difference 71
FT                   /note= "optionally substituted by Glu in human prolactin
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FT   Misc-difference 72
FT                   /note= "optionally substituted by Thr in human prolactin
FT                   variant of Claim 8"
FT   Misc-difference 75
FT                   /note= "optionally substituted by Lys in human prolactin
FT                   variant of Claim 8"
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FT   Misc-difference 76
FT               /note= "optionally substituted by Ser in human prolactin
FT               variant of Claim 8"
FT   Misc-difference 77
FT               /note= "optionally substituted by Asn in human prolactin
FT               variant of Claim 8"
FT   Misc-difference 78
FT               /note= "optionally substituted by Lys in human prolactin
FT               variant of Claim 8"
FT   Misc-difference 79
FT               /note= "optionally substituted by Glu in human prolactin
FT               variant of Claim 8"
FT   Misc-difference 180
FT               /note= "optionally substituted by Asp in human prolactin
FT               variant of Claim 8"
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FT               /note= "optionally substituted by Thr in human prolactin
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PN   US5955346-A.
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PD   21-SEP-1999.
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PF   07-JUN-1995;   95US-00476999.
XX
PR   28-OCT-1988;   88US-00264611.
PR   26-OCT-1989;   89US-00428066.
PR   27-APR-1992;   92US-00875204.
PR   13-OCT-1992;   92US-00960227.
PR   02-FEB-1994;   94US-00190723.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Cunningham BC, Wells JA;
XX
DR   WPI; 1999-560495/47.
XX
PT   Isolated nucleic acids encoding variants of human prolactin and placental
PT   lactogen useful for identifying active domains within those proteins.
XX
PS   Claim 7; Fig 2; 86pp; English.
XX
CC   This is the amino acid sequence of human prolactin. The invention
CC   provides a method for the systematic analysis of the structure and
CC   function of polypeptides by identifying active domains which influence
CC   the activity of the polypeptide with a target substance, and a method for
CC   identifying the active amino acid residues within the active domain of a
CC   polypeptide. It also provides polypeptide variants comprising segment-
CC   substituted and residue-substituted growth hormones, prolactins and
CC   placental lactogens. Claimed variants of human prolactin have 1-19 amino
CC   acid substitutions when compared to the wild-type sequence, selected from
CC   H59F, T60S, S61E, L63I, A64P, E67S, D68N, K69R, Q71E, A72T, M75K, N76S,
CC   Q77N, K78L, D79E, H180D, N184T, Y185F and K185R. These mutations
CC   inactivate the active domains and binding sites of the protein.
CC   Identifying receptor binding sites in hormones permits the rational
CC   design of receptor specific variants. Nucleic acids encoding the
CC   variants, expression vectors and host cells are also claimed
XX
SQ   Sequence 199 AA;

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AC   ABG94847;
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DT   03-DEC-2002  (first entry)
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DE   Human prolactin.
XX
KW   Growth hormone; placental lactogen; prolactin; active domain; hGH;
KW   structure-function relationship; segment-substituted polypeptide.
XX
OS   Homo sapiens.
XX
PN   US6428954-B1.
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PD   06-AUG-2002.
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PF   06-JUN-1995;   95US-00483039.
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PR   13-OCT-1992;   92US-00960227.
PR   02-FEB-1994;   94US-00190723.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Wells JA, Cunningham BC;
XX
DR   WPI; 2002-696875/75.
XX
PT   Identifying active domains within cloned polypeptides of known amino acid
PT   sequence by substituting analog segments into the parent polypeptide is
PT   useful to determine the relationship between structure and function.
XX
PS   Disclosure; Fig 2; 86pp; English.
XX
CC   The invention relates to identifying an unknown active domain in a region
CC   of known amino acid sequence in a parent polypeptide e.g. human growth
CC   hormone (hGH) which has been cloned and has a pre-identified biological
CC   activity, where the active domain interacts with a target when the parent
CC   polypeptide is in its native-folded form and the interaction is
CC   responsible for the biological activity comprising: (a) comparing the
CC   amino acid sequence or polypeptide structure in the region of known amino
CC   acid sequence of hGH with the amino acid sequence or polypeptide
CC   structure in a region of known amino acid sequence of an analogue
CC   polypeptide (e.g. prolactin, placental lactogen or porcine growth
CC   hormone) which has at least 15% homology with hGH alpha-carbon
CC   coordinates within about 2-3.5 angstroms of hGH alpha-carbon coordinates
CC   for about 60% of the analogue sequence, where any interaction of the
CC   analogue with the target is different from target interaction with hGH.
CC   (b) substituting DNA encoding an analogous polypeptide segment from the
CC   analogue into DNA encoding the full length hGH, and expressing a segment-
CC   substituted polypeptide; (c) contacting the segment-substituted
CC   polypeptide with the target to determine the interaction; (d) repeating steps
CC   (b) and (c) with a second analogous polypeptide segment; and (e)
CC   comparing the difference between activity of the first and second segment
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                    GenCore version 5.1.6
          Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:          September 13, 2004, 12:32:31 ; Search time 128 Seconds
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Total number of hits satisfying chosen parameters:          1335176

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Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.
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SUMMARIES

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2	199	100.0	200	10	US-09-819-094-9	Sequence 9, Appli
3	199	100.0	200	16	US-10-714-067-9	Sequence 25, Appli
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16	81	40.7	140	16	US-10-714-067-11	Sequence 11, Appl
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24	36	18.1	258	15	US-10-291-172-602	Sequence 30, Appl
25	31	15.6	31	14	US-10-140-293-30	Sequence 16, Appl
26	28	14.1	56	9	US-09-876-478-16	Sequence 20, Appl
27	26	13.1	199	14	US-10-140-293-20	Sequence 21, Appl
28	26	13.1	199	14	US-10-140-293-21	Sequence 24, Appl
29	26	13.1	199	14	US-10-140-293-24	Sequence 17, Appl
30	25	12.6	199	14	US-10-140-293-17	Sequence 22, Appl
31	25	12.6	199	14	US-10-140-293-22	Sequence 32, Appl
32	24	12.1	198	14	US-10-140-293-32	Sequence 26, Appl
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37	17	8.5	199	14	US-10-140-293-29	Sequence 13, Appl
38	14	7.0	197	14	US-10-140-293-13	Sequence 15, Appl
39	13	6.5	56	9	US-09-876-478-15	Sequence 14, Appl
40	13	6.5	197	14	US-10-140-293-14	Sequence 22, Appl
41	12	6.0	21	9	US-09-815-306-22	Sequence 29, Appl
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45	12	6.0	199	14	US-10-140-293-25	

ALIGNMENTS

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RESULT 1
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; Sequence 4, Application US/10153207
; Publication No. US20030153003A1
; GENERAL INFORMATION:
; APPLICANT: James A. Wells
; APPLICANT: Brian C. Cunningham
; TITLE OF INVENTION: GROWTH HORMONE VARIANTS
; FILE REFERENCE: 669.12-US-C7
; CURRENT APPLICATION NUMBER: US/10/153,207
; CURRENT FILING DATE: 2002-05-22
; PRIOR APPLICATION NUMBER: 08/479,884
; PRIOR FILING DATE: 1995-06-07
; PRIOR APPLICATION NUMBER: 08/190,723
; PRIOR FILING DATE: 1994-02-02
; PRIOR APPLICATION NUMBER: 07/960,227
; PRIOR FILING DATE: 1992-10-13
; PRIOR APPLICATION NUMBER: 07/875,204
; PRIOR FILING DATE: 1992-04-27
; PRIOR APPLICATION NUMBER: 07/428,066
; PRIOR FILING DATE: 1989-10-26
; PRIOR APPLICATION NUMBER: 07/264,611
; PRIOR FILING DATE: 1988-10-28
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: FastSEQ for Windows Version 4.0
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; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-153-207-4

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; Sequence 9, Application US/09819094
; Publication No. US20030186382A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, Richard I.
; APPLICANT: Martial, Joseph A.
; APPLICANT: Struman, Ingrid
; APPLICANT: Taylor, Robert
; APPLICANT: Bentzien, Frauke
; TITLE OF INVENTION: No. US2003018638282A1e1 Antiangiogenic Peptide Agents and Their
; TITLE OF INVENTION: Therapeutic and Diagnostic Use
; FILE REFERENCE: UCSF-018/02US
; CURRENT APPLICATION NUMBER: US/09/819,094
; CURRENT FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/076,675
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/046,394
; PRIOR FILING DATE: 1997-05-12
; NUMBER OF SEQ ID NOS: 34
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US-09-819-094-9

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US-10-714-067-9
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; Publication No. US2004007705A1
; GENERAL INFORMATION:
; APPLICANT: Weiner, Richard I.
; APPLICANT: Martial, Joseph A.
; APPLICANT: Struman, Ingrid
; APPLICANT: Taylor, Robert
; APPLICANT: Bentzien, Frauke
; TITLE OF INVENTION: Novel Antiangiogenic Peptide Agents and Their
; TITLE OF INVENTION: Therapeutic and Diagnostic Use
; FILE REFERENCE: UCSF-018/02US
; CURRENT APPLICATION NUMBER: US/10/714,067
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US/09/819,094
; PRIOR FILING DATE: 2001-03-27
; PRIOR APPLICATION NUMBER: 09/076,675
; PRIOR FILING DATE: 1998-05-12
; PRIOR APPLICATION NUMBER: 60/046,394
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; ORGANISM: Homo sapiens
US-10-714-067-9

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; Sequence 1, Application US/09815306
; Patent No. US2002006804A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, WEN Y.
; APPLICANT: WAGNER, THOMAS E.
; TITLE OF INVENTION: BI-FUNCTIONAL CANCER TREATMENT AGENTS
; FILE REFERENCE: 035879/0120
; CURRENT APPLICATION NUMBER: US/09/815,306
; CURRENT FILING DATE: 2001-03-23
; PRIOR APPLICATION NUMBER: 60/191,457
; PRIOR FILING DATE: 2000-03-23
; NUMBER OF SEQ ID NOS: 33
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           GenCore version 5.1.6
     Copyright (c) 1993 - 2004 Compugen Ltd.

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

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4	1043	100.0	970	7	ACA56818	Aca56818 Signallin
5	1043	100.0	1062	5	AAS44957	Aas44957 cDNA enco
6	1043	100.0	1071	2	AAZ41975	Aaz41975 Human myo
7	1043	100.0	1100	2	AAQ96139	Aaq96139 Prolactin
8	1036	99.3	5278	2	AAQ05168	Aaq05168 Plasmid p
9		99.1	1034	832	1	AAN80115	Aan80115 Human pre
10		99.0	1033	600	2	AAT74325	Aat74325 cDNA enco
11		98.8	1031	3621	7	AAN60847	Aan60847 Human pre
12		97.9	1021.5	1066	2	AAL51964	Aal51964 Human ext
13		96.5	1006	832	2	AAT74333	Aat74333 cDNA enco
14		96.1	1002	603	7	AAX01697	Aax01697 Human ant
15		79.1	825	688	7	ABZ83636	Abz83636 Toxicolog
16 c		76.4	797	804	6	ABL51716	Abl51716 Bovine pr
17		76.4	797	3628	1	AAN60848	Aan60848 Plasmid s
18		76.1	794	926	7	ACC69735	Acc69735 Ovine pro
19		72.9	760.5	889	7	AAL51963	Aal51963 Human ext
20		72.3	754	600	2	AAT03456	Aat03456 Turkey pr
21		72.3	754	1281	2	AAT03457	Aat03457 Turkey pr
22		71.7	748	3926	2	AAQ03736	Aaq03736 Sequence
23		68.1	710	818	7	AAL51960	Aal51960 Human ext
24		67.6	705	423	2	AAX01696	Aax01696 Human ant
25		66.1	689.5	657	1	AAN70832	Aan70832 Cattle re
26		64.0	667	899	2	AAQ14451	Aaq14451 Rat prola
27		64.0	667	3735	2	AAQ14452	Aaq14452 Rat prola
28		63.2	659	594	2	AAT74324	Aat74324 cDNA enco
29		62.9	656	822	1	AAN80114	Aan80114 Rat prepr
30		61.5	641	390	2	AAX58737	Aax58737 DNA encod
31		61.5	641	771	2	AAX58738	Aax58738 DNA encod
32		61.0	636	375	2	AAV10505	Aav10505 Human pro
33		61.0	636	754	2	AAV10506	Aav10506 Human con
34		60.0	626	375	2	AAX01695	Aax01695 Human ant
35		59.3	619	681	2	AAQ13553	Aaq13553 Prolactin
36		55.0	574	445	7	ABX39876	Abx39876 Bovine ES
37		54.5	568	437	7	ABX40855	Abx40855 Bovine ES
38		54.1	564	1290	7	AAQ15023	Aaq15023 Rat prola
39		53.2	555	433	7	ABX46016	Abx46016 Bovine ES
40		52.5	548	431	7	ABX38684	Abx38684 Bovine ES
41		52.2	544	428	7	ABX41798	Abx41798 Bovine ES
42		52.1	543	435	7	ABX43432	Abx43432 Bovine ES
43		52.0	542	437	7	ABX42234	Abx42234 Bovine ES
44		51.3	535	436	7	ABX37481	Abx37481 Bovine ES
45		51.2	534	417	7	ABX42247	Abx42247 Bovine ES

ALIGNMENTS

RESULT 1
AAX01694
ID   AAX01694 standard; DNA; 603 BP.
XX
AC   AAX01694;
XX
DT   08-JUN-1999 (first entry)
XX
DE   Human anti-angiogenic hPRL Met-1Cys199 DNA.
XX
KW   Human; anti-angiogenic; prolactin; placental lactogen; hPL; angiogenesis;
KW   growth hormone; hGH; hGH-V; capillary endothelial cell proliferation;
KW   placental vascularisation; pregnancy; treatment; angiogenic disease;
KW   tumour; inhibitor; malignant; angiofibroma; arteriovenous malformation;
KW   arthritis; atherosclerotic plaques; corneal graft neovascularisation;
KW   wound healing; proliferative retinopathy; macular degeneration; trachoma;
KW   granulation; glaucoma; ocular; uveitis; fracture; Osler-Weber syndrome;
KW   psoriasis; fibroplasia; scleroderma; Kaposi's sarcoma; vascular adhesion;
KW   ulcer; leukaemia; reproductive disorder; contraceptive agent;
KW   gene therapy; pre-eclampsia; intrauterine growth retardation;
KW   placental dysfunction; ss.
XX
OS   Homo sapiens.
XX
PN   WO9851323-A1.
XX
PD   19-NOV-1998.
XX
PF   12-MAY-1998; 98WO-US009691.
XX
PR   13-MAY-1997; 97US-0046394P.
XX

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Db    244  CTGAGCCTGATAGTCAGCATATTGCGATCCTGGATGAGCCTCTGTATCATCTGTCACG  303
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Qy    101  GluValArgGlyMetGlnArgIleLeuAlaProGluAlaIleLeuSerLysAlaValGluIleGlu  120

Db    304  GAAGTACGTGGTATGCAAGAAGCCCGAGGCTATCCTATCCAAAGCTGTAGAGATTGAG  363
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Qy    121  GluIleGlnThrLysArgLeuLeuGlyMetGluGluValSerGlnValHisProGlu  140

Db    364  GAGCAAACCAAACGGCTTCTAGAGGGCATGGAGTCAGTAGTCAGGTTCATCCTGAA  423
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Qy    141  ThrLysGluAsnIleTyrProValTrpSerGlyLeuProSerLeuGlnMetAlaAsp  160

Db    424  ACCAAAGAAAATGAGATCACCCCTGTCTGGTCGGGACTTCCATCCTCGAGATGGCTGAT  483
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Qy    161  GlyGluSerArgLeuSerAlaTyrTyrAsnLeuLeuHisCysLeuArgArgAspSerHis  180

Db    484  GAAGAGTCTCGCCTTTCTGCTTATTATAAACCTGCTCCACTGCCTACGCAGGGATTCACAT  543
           |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy    181  LysIleAspAsnTyrLeuLysLeuLeuLysCysArgIleIleHisAsnAsnAsnCys  199

Db    544  AAAATCGACAATTATCTCAAGCTCCTGAAGTGCCGAATCATCCACAACAACAACTGC  600
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RESULT 2
ABV94102
ID   ABV94102 standard; cDNA; 833 BP.
XX
AC   ABV94102;
XX
DT   08-JAN-2003 (first entry)
XX
DE   Breast carcinoma related nucleotide sequence SEQ ID NO:93.
XX
KW   Human; breast carcinoma; cancer; tumour; cytostatic; anti-tumour; gene;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   WO200246467-A2.
XX
PD   13-JUN-2002.
XX
PF   07-DEC-2001; 2001WO-IB002811.
XX
PR   08-DEC-2000; 2000US-0254090P.
PR   07-DEC-2001; 2001US-00007926.
XX
PA   'IPSO-) IPSOGEN.
XX
PI   Bertucci F, Houlgatte R, Birnbaum D, Nguyen C, Viens P, Fert V;
XX
DR   WPI; 2002-619023/66.
XX
PT   Novel polynucleotide library useful in molecular characterization of a
PT   carcinoma, comprising a pool of polynucleotide sequences or its
PT   subsequences which are either underexpressed or overexpressed in tumor
PT   cells.
XX
PS   Claim 1; Page 172; 401pp; English.
XX
CC   The present invention describes a polynucleotide library (I) useful in
CC   the molecular characterisation of a carcinoma, comprising a pool of
CC   polynucleotides or its subsequences which are either underexpressed or
CC   overexpressed in tumour cells, and correspond to any of the
CC   polynucleotide sequences chosen from the 468 sequences given in ABV94010
CC   to ABV94477. Also described: (1) a polynucleotide array (III) useful for
CC   the prognosis or diagnostic of tumour, comprising (I); and (2) detecting
CC   (M1) differentially expressed polynucleotide sequences which are
CC   correlated with a cancer, involves obtaining a polynucleotide sample from
CC   a patient, and reacting the polynucleotide sample obtained with a probe
CC   immobilised on a solid support, where the probe comprises any combination
CC   of the polynucleotide sequences of (I) or its expression products encoded
CC   by polynucleotide sequences of (I), and detecting the reaction product.
CC   (I) have cytostatic activities and can be used as anti-tumour agents. (I)

PA   (REGC) UNIV CALIFORNIA.
XX
PI   Weiner RI, Martial JA, Struman I, Taylor R;
XX
DR   WPI; 1999-045192/04.
DR   P-PSDB; AAW92258.
XX
PT   New anti-angiogenic peptides - comprise N-terminal fragments of human
PT   placental lactogen, human growth hormone, growth hormone variant or human
PT   prolactin.
XX
PS   Example 3; Page 41; 87pp; English.
XX
CC   This invention describes novel human anti-angiogenic peptides derived
CC   from 10 to 150 consecutive amino acids selected from the N-terminal end
CC   of human placental lactogen (hPL), human growth hormone (hGH) growth
CC   hormone variant (hGH-V), or human prolactin. Such peptides (i) inhibit
CC   capillary endothelial cell proliferation and organisation (ii) inhibit
CC   angiogenesis in chick chorioallantoic membrane and (iii) binds to at
CC   least one specific receptor which does not bind an intact full length
CC   hGH, hPL, prolactin or hGH-v. The invention also describes a method for
CC   diagnosing a probable abnormality of placental vascularisation during
CC   pregnancy. The peptides can be used for treating an angiogenic disease in
CC   a subject, for inhibiting tumour formation or growth in a patient or for
CC   modulating vascularisation of a patient's placenta. In particular, the
CC   peptides can be used for preventing or treating e.g. malignant tumours,
CC   angiofibroma, arteriovenous malformation, arthritis such as rheumatoid
CC   arthritis, atherosclerotic plaques, corneal graft neovascularisation,
CC   delayed wound healing, proliferative retinopathy such as diabetic
CC   retinopathy, macular degeneration, granulations such as those occurring
CC   in haemophilic joints, inappropriate vascularisation in wound healing
CC   such as hypertrophic scars or keloid scars, neovascular glaucoma, ocular
CC   tumour, uveitis, non-union fractures, Osler-Weber syndrome, psoriasis,
CC   pyogenic glaucoma, retrolental fibroplasia, scleroderma, solid tumours,
CC   Kaposi's sarcoma, trachoma, vascular adhesions, chronic varicose ulcers,
CC   leukaemia, and reproductive disorders such as follicular and luteal cysts
CC   and choriocarcinoma. They can also be used as contraceptive agents. DNA
CC   encoding the peptides can be used in gene therapy. The measurement of
CC   abnormal levels of N-terminal fragments of hGH, hGH-v, prolactin or hPL
CC   can be used in assays for impairment of vascular development associated
CC   with pre-eclampsia, intrauterine growth retardation, and placental
CC   dysfunction
XX
SQ   Sequence 603 BP; 161 A; 173 C; 134 G; 135 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:   1.44e-102   Length: 603
Score: 1043.00   Matches: 199
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: 2   Gaps: 0

US-10-735-594-1 (1-199) x AAX01694 (1-603)

Qy   1 LeuProIleCysProGlyGlyValAlaAlaArgCysGlnValThrLeuArgAspLeuPheAsp   20
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Qy   21 ArgAlaValAlaLeuSerHisTyrIleHisTyrIleHisAsnLeuSerSerGluMetPheSerGluPhe   40
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Db   64 CGCGCCGTGCGTCCTGCTCCCACTACATCCATAACCTTCCTCCAGAAATGTTCAGCGAATTC   123

Qy   41 AspLysArgTyrThrHisGlyArgGlyPheIleThrLysAsnSerAlaIleAsnSerCysHisThr   60
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Db   124 GATAAACGGTATACCCATGGCCGGGGTTCATTACCAAGGCCATCAACAGCTCCACACT   183

Qy   61 SerSerLeuAlaThrProGluAspLysGluGlnAlaGlnGlnMetAsnGlnLysAspPhe   80
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Db   184 TCTTCCCTTGCCACCCCGAAGACAAGGAGCAAGCCCAACAGATGAATCAAAAAGACTTT   243

Qy   81 LeuSerLeuIleValSerIleLeuArgSerTrpAsnGluProLeuTyrHisLeuValThr 100
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            GenCore version 5.1.6
    Copyright (c) 1993 - 2004  Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:     September 13, 2004, 17:29:24 ; Search time 494 Seconds
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Title:          US-10-735-594-1
Perfect score:  1043
Sequence:       1 LPICPGGAARCQVTLRDLFD.........HKIDNYLKLLKCRIIHNNNC 199

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        Fgapop   6.0 , Fgapext   7.0
        Delop    6.0 , Delext    7.0

Searched:   3304383 seqs, 251761380 residues

Total number of hits satisfying chosen parameters:       6608766

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
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 -DB=Published_Applications_NA -QFMT=fastap -SUFFIX=p2n.rnpb -MINMATCH=0.1
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 -TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100
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 -MAXLEN=200000000 -USER=US10735594 @CGN 1_1_912 @runat 10092004_144655_5672
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Database :   Published_Applications_NA:
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    2: /cgn2_6/ptodata/2/pubpna/PCT_NEW_PUB.seq:
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result   %
No.   Score Match Query Length DB ID   Description

No.	Score	% Match	Query	Length	DB	ID	Description
1	1043	100.0	684	15	US-10-140-293-1	Sequence 1, Appli
2	1043	100.0	833	15	US-10-007-926A-93	Sequence 93, Appl
3	1043	100.0	970	16	US-10-305-720-1416	Sequence 1416, Ap
4	1043	100.0	1062	13	US-10-221-278-38	Sequence 38, Appl
5	1043	100.0	1062	16	US-10-291-172-38	Sequence 38, Appl
6	1043	100.0	1097	15	US-10-119-428-41	Sequence 41, Appl
7	1039	99.6	832	13	US-09-065-330D-1	Sequence 1, Appli
8	1036	99.3	603	10	US-09-819-094-1	Sequence 1, Appli
9	1036	99.3	603	10	US-10-714-067-1	Sequence 1, Appli
10	1035	99.2	603	17	US-10-449-609-2	Sequence 2, Appli
11	1035	99.2	684	15	US-10-140-293-2	Sequence 2, Appli
12	1035	99.2	1158	17	US-10-449-609-5	Sequence 5, Appli
13	1002	96.1	603	10	US-09-819-094-4	Sequence 4, Appli
14	1002	96.1	603	17	US-10-714-067-4	Sequence 4, Appli
15	748	71.7	642	13	US-10-424-599-133827	Sequence 133827,
16	705	67.6	423	10	US-09-819-094-3	Sequence 3, Appli
17	705	67.6	423	17	US-10-714-067-3	Sequence 3, Appli
18	641	61.5	390	14	US-10-036-869-26	Sequence 26, Appl
19	641	61.5	771	14	US-10-036-869-28	Sequence 28, Appl
20	626	60.0	375	17	US-09-819-094-2	Sequence 2, Appli
21	626	60.0	375	17	US-10-714-067-2	Sequence 2, Appli
22	574	55.0	445	9	US-09-960-352-5041	Sequence 5041, Ap
23	568	54.5	437	9	US-09-960-352-6020	Sequence 6020, Ap
24	555	53.2	433	9	US-09-960-352-11181	Sequence 11181, A
25	548	52.5	431	9	US-09-960-352-3849	Sequence 3849, Ap
26	544	52.2	428	9	US-09-960-352-6963	Sequence 6963, Ap
27	543	52.1	435	9	US-09-960-352-8597	Sequence 8597, Ap
28	542	52.0	437	9	US-09-960-352-7399	Sequence 7399, Ap
29	535	51.3	436	9	US-09-960-352-2646	Sequence 2646, Ap
30	534	51.2	417	9	US-09-960-352-7412	Sequence 7412, Ap
31	524	50.2	438	9	US-09-960-352-4342	Sequence 4342, Ap
32	517	49.6	437	9	US-09-960-352-6489	Sequence 6489, Ap
33	515	49.4	415	9	US-09-960-352-7192	Sequence 7192, Ap
34	501	48.0	416	9	US-09-960-352-9977	Sequence 9977, Ap
35	499	47.8	406	9	US-09-960-352-14730	Sequence 14730, A
36	495	47.5	410	9	US-09-960-352-778	Sequence 778, Ap
37	491	47.1	433	9	US-09-960-352-5287	Sequence 5287, Ap
38	491	47.1	439	9	US-09-960-352-9982	Sequence 9982, Ap
39	491	47.1	439	9	US-09-960-352-13557	Sequence 13557, A
40	482	46.2	417	9	US-09-960-352-3145	Sequence 3145, Ap
41	479	45.9	425	9	US-09-960-352-3594	Sequence 3594, Ap
42	475	45.5	398	9	US-09-960-352-9300	Sequence 9300, Ap
43	473	45.3	424	9	US-09-960-352-9737	Sequence 9737, Ap
44	466	44.7	378	9	US-09-960-352-4347	Sequence 4347, Ap
45	463	44.4	363	9	US-09-960-352-6004	Sequence 6004, Ap

ALIGNMENTS

RESULT 1
US-10-140-293-1
; Sequence 1, Application US/10140293
; Publication No. US20030022833A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, WEN Y.
; APPLICANT: WAGNER, THOMAS E.
; TITLE OF INVENTION: USE OF ANTI-PROLACTIN AGENTS TO TREAT PORLIFERATIVE
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 035879/0109
; CURRENT APPLICATION NUMBER: US/10/140,293
; CURRENT FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US/09/246,041
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn Ver. 2.1
;
; SEQ ID NO 1
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-140-293-1

Alignment Scores:

; FEATURE:
; OTHER INFORMATION: prolactin (PRL) gene.
US-10-007-926A-93

Alignment Scores:
Pred. No.:   2.18e-129   Length: 833
Score: 1043.00   Matches: 199
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 15   Indels: 0
DB: Gaps: 0

US-10-735-594-1 (1-199) x US-10-007-926A-93 (1-833)

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Db   89 TTGCCATCTGTCCCGGCGGGGCTGCCCGATGCCAGGTGACCCTTGCGAGACCCTGTTTGAC  148

Qy   21 ArgAlaValValLeuSerHisTyrIleHisAsnLeuSerSerGluMetPheSerGluPhe   40
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Db  149 CGGGCCGTCGTCCTGTCCCACTACATCCATAACCTCTCCTCCGAGAAATGTTCAGGGAATTC  208

Qy   41 AspLysArgTyrThrHisGlyPheIleThrLysAlaIleAlaSerCysHisThr   60
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Qy   61 AspLysArgTyrThrHisGlyArgGlyPheIleThrLysAlaIleAlaSerCysHisThr   60
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Db  269 TCTTCCCTTGCCACCCCCGAAGACAAGGAGCCCAACAGATGAATCAAAAAGACTTT  328

Qy   81 LeuSerLeuIleValSerIleLeuArgSerTrpAsnGluProLeuTyrHisLeuValThr  100
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Db  329 CTGAGCCTGATAGTCAGCATATTGCGATCCTGGAATGGACCCTCTGTATCATCTGGTCACG  388

Qy  101 GluValArgGlyMetGlnGluAlaProGluAlaIleLeuSerLysAlaValGluIleGlu  120
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Db  389 GAAGTACGTGGTATGCAAGAAGCCCCGGAGGCTATCCTATCCAAAGCTGTAGAGATTGAG  448

Qy  121 GlyGlnThrLysArgLeuLeuGluGlyMetGluLeuIleValSerGlnValSerProGlu  140
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Db  449 GAGCAAACCAAACGGCTTCTAGAGGGCATGGAGCTGATAGTCAGCCAGGTTCATCCTGAA  508

Qy  141 ThrLysGluAsnGluIleTyrProValTrpSerGlyLeuProSerGlyGlnMetAlaAsp  160
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Db  509 ACCAAAGAAAATGAGATCTACCCGTGTCGTCGGGACTTCCATCCCTGCAGATGGCTGAT  568

Qy  161 GluGluSerArgLeuSerAlaTyrTyrAsnLeuLeuHisCysLeuArgArgAspSerHis  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  569 GAAGAGTCTCGCCTTTCTGCTTATTATAACCTGCTCCACTGCCTCACGCAGGATTCACAT  628

Qy  181 LysIleAspAsnTyrLeuLysLeuLeuLysCysArgIleIleHisAsnAsnCys  199
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  629 AAAATCGACAATTATCTCAAGCTCCTGAAGTGCCGAATCATCCACAACAACTGC  685
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RESULT 3
US-10-305-720-1416
; Sequence 1416, Application US/10305720
; Publication No. US20040010136A1
; GENERAL INFORMATION:
; APPLICANT: Au-Young, Janice K.; Seilhamer, Jeffrey J.
; TITLE OF INVENTION: Composition for the Detection of Signaling Pathway Gene Expressi
; FILE REFERENCE: PA-0002-1 CON
; CURRENT APPLICATION NUMBER: US/10/305,720
; CURRENT FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 09/016,434
; PRIOR FILING DATE: 1998-01-30
; NUMBER OF SEQ ID NOS: 1490
; SOFTWARE: PERL Program
; SEQ ID NO 1416
; LENGTH: 970
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:

Pred. No.:   1.59e-129   Length: 684
Score: 1043.00   Matches: 199
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 15   Indels: 0
DB: Gaps: 0

US-10-735-594-1 (1-199) x US-10-140-293-1 (1-684)

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Qy    1 LeuProIleCysProGlyGlyAlaAlaArgCysGlnValThrLeuArgAspLeuPheAsp   20
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   85 TTGCCATCTGTCCCGGCGGGGCTGCCCGATGCCAGGTGACCCTTGCGAGACCCTGTTTGAC  144

Qy   21 ArgAlaValValLeuSerHisTyrIleHisAsnLeuSerSerGluMetPheSerGluPhe   40
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  145 CGGGCCGTCGTCCTGTCCCACTACATCCATAACCTCTCCTCCGAGAAATGTTCAGCGAATTC  204

Qy   41 AspLysArgTyrThrHisGlyPheIleThrLysAlaIleAlaSerCysHisThr   60
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  205 GATAAAACGGTATACCCATGGCCCGGGGGTTCATTACCAAGGCCATCAACAGCTGCCACACT  264

Qy   61 SerSerLeuAlaThrProGluAspLysGluGlnAlaGlnGlnMetAsnGlnLysAspPhe   80
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  265 TCTTCCCTTGCCACCCCCGAAGACAAGGAGCCCAACAGATGAATCAAAAAGACTTT  324

Qy   81 LeuSerLeuIleValSerIleLeuArgSerTrpAsnGluProLeuTyrHisLeuValThr  100
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  325 CTGAGCCTGATAGTCAGCATATTGCGATCCTGGAATGGACCCTCTGTATCATCTGGTCACG  384

Qy  101 GluValArgGlyMetGlnGluAlaProGluAlaIleLeuSerLysAlaValGluIleGlu  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  385 GAAGTACGTGGTATGCAAGAAGCCCCGGAGGCTATCCTATCCAAAGCTGTAGAGATTGAG  444

Qy  121 GlyGlnThrLysArgLeuLeuGluGlyMetGluLeuIleValSerGlnValHisProGlu  140
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  445 GAGCAAACCAAACGGCTTCTAGAGGGCATGGAGCTGATAGTCAGCCAGGTTCATCCTGAA  504

Qy  141 ThrLysGluAsnGluIleTyrProValTrpSerGlyLeuProSerGlyGlnMetAlaAsp  160
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  505 ACCAAAGAAAATGAGATCTACCCGTGTCGTCGGGACTTCCATCCCTGCAGATGGCTGAT  564

Qy  161 GluGluSerArgLeuSerAlaTyrTyrAsnLeuLeuHisCysLeuArgArgAspSerHis  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  565 GAAGAGTCTCGCCTTTCTGCTTATTATAACCTGCTCCACTGCCTCACGCAGGATTCACAT  624

Qy  181 LysIleAspAsnTyrLeuLysLeuLeuLysCysArgIleIleHisAsnAsnCys  199
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  625 AAAATCGACAATTATCTCAAGCTCCTGAAGTGCCGAATCATCCACAACAACTGC  681
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RESULT 2
US-10-007-926A-93
; Sequence 93, Application US/10007926A
; Publication No. US2003014153Al
; GENERAL INFORMATION:
; APPLICANT: BERTUCCI, FRANCOIS
; APPLICANT: HOULGATTE, REMI
; APPLICANT: BIRNBAUM, DANIEL
; APPLICANT: NGUYEN, CATHERINE
; APPLICANT: VIENS, PATRICE
; APPLICANT: FERT, VINCENT
; TITLE OF INVENTION: GENE EXPRESSION PROFILING OF PRIMARY BREAST CARCINOMAS
; TITLE OF INVENTION: USING ARRAYS OF CANDIDATE GENES
; FILE REFERENCE: 1546-R-00
; CURRENT APPLICATION NUMBER: US/10/007,926A
; CURRENT FILING DATE: 2001-12-07
; PRIOR APPLICATION NUMBER: 60/254,090
; PRIOR FILING DATE: 2000-12-08
; NUMBER OF SEQ ID NOS: 468
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 93
; LENGTH: 833
; TYPE: DNA
; ORGANISM: Homo sapiens

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; NAME/KEY: misc feature
; OTHER INFORMATION: GenBank ID No. US20040010136A1 g531102
US-10-305-720-1416

Alignment Scores:
Pred. No.:             2.78e-129      Length:          970
Score:                 1043.00        Matches:         199
Percent Similarity:    100.00%        Conservative:    0
Best Local Similarity: 100.00%        Mismatches:      0
Query Match:           100.00%        Indels:          0
DB:                                   Gaps:            16

US-10-735-594-1 (1-199) x US-10-305-720-1416 (1-970)

Qy   1 LeuProIleCysProGlyGlyAlaAlaArgCysGlnValThrLeuArgAspLeuPheAsp 20
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 226 TTGCCCATCTGTCCCGGCGGCGCTGCCCGATGCCCAGGTGACCCTTCGAGACCTGTTTGAC 285

Qy  21 ArgAlaValValLeuSerHisTyrIleHisAsnLeuSerSerGluMetPheSerGluPhe 40
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 286 CGCGCCGTGGTCCTGTCCCACTACATCCATAACCTCTCTCAGAAATGTTCAGCGAATTC 345

Qy  41 AspLysArgTyrThrHisGlyArgGlyPheIleThrLysAlaIleAsnSerCysHisThr 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 346 GATAAAACGGTATACCCATGGCCGGGGGTTCATTACCAAGGCCATCAACAGCTGCCACACT 405

Qy  61 SerSerLeuAlaThrProGluAspLysGlyGlnAlaGlnMetAsnGlnLysAspPhe 80
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 406 TCTTCCCTTGCCACCCCCGAAGACAAGGAGCAAGGCCAACAGATGAATCAAAAAGACTTT 465

Qy  81 LeuSerLeuIleValSerIleLeuArgSerTrpAsnGluProLeuTyrHisLeuValThr 100
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 466 CTGAGCCTGATAGTCAGCATATTGCGATCCTGGAATGAGCCTCTGTATCATCTGGTCACG 525

Qy 101 GluValArgGlyMetGlnGluAlaProGluAlaIleLeuSerLysAlaValGluIleGlu 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 526 GAAGTACGTGGTATGCAAGAAGCCCCCGAGGCTATCCTATCCAAAGCTGTAGAGATTGAG 585

Qy 121 GluGlnThrLysArgLeuLeuGluGlyMetGluLeuValSerGlnValHisProGlu 140
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 586 GAGCAAACCAAACGGCTTCTAGAGGGCATGGAGCTGGTCAGCCAGGTTCATCCTGAA 645

Qy 141 ThrLysGluAsnGluIleTyrProValTrpSerGlyLeuProSerLeuGlnMetAlaAsp 160
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 646 ACCAAAGAAAATGAGATCTACCCTGTCTGGTCGGGACTTCCATCCCTGCAGATGGCTGAT 705

Qy 161 GluGluSerArgLeuSerAlaTyrTyrAsnLeuLeuHisCysLeuArgArgAspSerHis 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 706 GAAGAGTCTCGCCTTTCTGCTTATTATAACCTGCTCCACTGCCTACGCAGGGATTCACAT 765

Qy 181 LysIleAspAsnTyrLeuLysLeuLeuLysCysArgIleIleHisAsnAsnAsnCys 199
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 766 AAAATCGACAATTATCTCAAGCTCCTGAAGTGCCGAATCATCCACAACAACAACTGC 822

RESULT 4
US-10-221-278-38
; Sequence 38, Application US/10221278
; Publication No. US20040034208A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
; TITLE OF INVENTION: No. US20040034208A1e1 Nucleic Acids and Polypeptides
; FILE REFERENCE: 21272-045
; CURRENT APPLICATION NUMBER: US/10/221,278
; CURRENT FILING DATE: 2002-09-06
; PRIOR APPLICATION NUMBER: 09/693,267
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/665,363
; PRIOR FILING DATE: 2000-09-19
; PRIOR APPLICATION NUMBER: 09/616,847
; PRIOR FILING DATE: 2000-07-14
; PRIOR APPLICATION NUMBER: 09/596,193
; PRIOR FILING DATE: 2000-06-17
; PRIOR APPLICATION NUMBER: 09/574,454
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; PRIOR FILING DATE: 2000-05-19
; PRIOR APPLICATION NUMBER: 09/519,705
; PRIOR FILING DATE: 2000-03-07
; NUMBER OF SEQ ID NOS: 752
; SEQ ID NO 38
; LENGTH: 1062
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (140)..(820)
; FEATURE:
; NAME/KEY: misc_feature
; LOCATION: (1)..(1062)
; OTHER INFORMATION: n = a,t,c or g
US-10-221-278-38

Alignment Scores:
Pred. No.:             3.22e-129      Length:          1062
Score:                 1043.00        Matches:         199
Percent Similarity:    100.00%        Conservative:    0
Best Local Similarity: 100.00%        Mismatches:      0
Query Match:           100.00%        Indels:          0
DB:                                   Gaps:            13

US-10-735-594-1 (1-199) x US-10-221-278-38 (1-1062)

Qy   1 LeuProIleCysProGlyGlyAlaAlaArgCysGlnValThrLeuArgAspLeuPheAsp 20
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 224 TTGCCCATCTGTCCCGGCGGCGCTGCCCGATGCCCAGGTGACCCTTCGAGACCTGTTTGAC 283

Qy  21 ArgAlaValValLeuSerHisTyrIleHisAsnLeuSerSerGluMetPheSerGluPhe 40
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 284 CGCGCCGTGGTCCTGTCCCACTACATCCATAACCTCTCTCAGAAATGTTCAGCGAATTC 343

Qy  41 AspLysArgTyrThrHisGlyArgGlyPheIleThrLysAlaIleAsnSerCysHisThr 60
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 344 GATAAAACGGTATACCCATGGCCGGGGGTTCATTACCAAGGCCATCAACAGCTGCCACACT 403

Qy  61 SerSerLeuAlaThrProGluAspLysGlyGlnAlaGlnMetAsnGlnLysAspPhe 80
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 404 TCTTCCCTTGCCACCCCCGAAGACAAGGAGCAAGGCCAACAGATGAATCAAAAAGACTTT 463

Qy  81 LeuSerLeuIleValSerIleLeuArgSerTrpAsnGluProLeuTyrHisLeuValThr 100
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 464 CTGAGCCTGATAGTCAGCATATTGCGATCCTGGAATGAGCCTCTGTATCATCTGGTCACG 523

Qy 101 GluValArgGlyMetGlnGluAlaProGluAlaIleLeuSerLysAlaValGluIleGlu 120
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 524 GAAGTACGTGGTATGCAAGAAGCCCCCGAGGCTATCCTATCCAAAGCTGTAGAGATTGAG 583

Qy 121 GluGlnThrLysArgLeuLeuGluGlyMetGluLeuValSerGlnValHisProGlu 140
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 584 GAGCAAACCAAACGGCTTCTAGAGGGCATGGAGCTGGTCAGCCAGGTTCATCCTGAA 643

Qy 141 ThrLysGluAsnGluIleTyrProValTrpSerGlyLeuProSerLeuGlnMetAlaAsp 160
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 644 ACCAAAGAAAATGAGATCTACCCTGTCTGGTCGGGACTTCCATCCCTGCAGATGGCTGAT 703

Qy 161 GluGluSerArgLeuSerAlaTyrTyrAsnLeuLeuHisCysLeuArgArgAspSerHis 180
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 704 GAAGAGTCTCGCCTTTCTGCTTATTATAACCTGCTCCACTGCCTACGCAGGGATTCACAT 763

Qy 181 LysIleAspAsnTyrLeuLysLeuLeuLysCysArgIleIleHisAsnAsnAsnCys 199
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db 764 AAAATCGACAATTATCTCAAGCTCCTGAAGTGCCGAATCATCCACAACAACAACTGC 820

RESULT 5
US-10-291-172-38
; Sequence 38, Application US/10291172
; Publication No. US20030228584A1
; GENERAL INFORMATION:
; APPLICANT: Hyseq, Inc
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;  TITLE OF INVENTION: No. US20030228584Alel Nucleic Acids and Polypeptides
;  FILE REFERENCE: 21272-045
;  CURRENT APPLICATION NUMBER: US/10/291,172
;  CURRENT FILING DATE: 2000-11-08
;  PRIOR APPLICATION NUMBER: 09/693,267
;  PRIOR FILING DATE: 2000-10-20
;  PRIOR APPLICATION NUMBER: 09/665,363
;  PRIOR FILING DATE: 2000-09-19
;  PRIOR APPLICATION NUMBER: 09/616,847
;  PRIOR FILING DATE: 2000-07-14
;  PRIOR APPLICATION NUMBER: 09/596,193
;  PRIOR FILING DATE: 2000-06-17
;  PRIOR APPLICATION NUMBER: 09/574,454
;  PRIOR FILING DATE: 2000-05-19
;  PRIOR APPLICATION NUMBER: 09/519,705
;  PRIOR FILING DATE: 2000-03-07
;  NUMBER OF SEQ ID NOS: 752
;  SEQ ID NO 38
;  LENGTH: 1062
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (140)..(820)
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: (1)...(1062)
;  OTHER INFORMATION: n = a,t,c or g
US-10-291-172-38

Alignment Scores:
Pred. No.:
Score:                    3.22e-129       Length:         1062
Percent Similarity:       1043.00         Matches:        199
Best Local Similarity:    100.00%         Conservative:   0
Query Match:              100.00%         Mismatches:     0
DB:                       16              Indels:         0
                                          Gaps:           0

US-10-735-594-1 (1-199) x US-10-291-172-38 (1-1062)

Qy   1 LeuProIleCysProGlyGlyValGlyAlaAlaArgCysGlnValThrLeuArgAspLeuPheAsp  20
Db 224 TTGCCCATCTGTCCGGCGGGGCTGCCCGATGCCAGGTGACCCTTCGAGACCTGTTTGAC        283

Qy  21 ArgAlaValValLeuSerHisTyrIleHisAsnLeuSerGluMetPheSerGluPhe          40
Db 284 CGCGCCGTCGTCCTGTCCCACTACATCCATAACCTCTCCGAAATGTTCAGCGAATTC         343

Qy  41 AspLysArgGlyTyrThrHisGlyArgGlyPheIleThrLysAsnSerCysHisThr          60
Db 344 GATAAACGGTATACCCATGGCCGGGGGTTCATTACCAAGGCCATCAACAGCTGCCACACT      403

Qy  61 SerSerLeuAlaThrProGluAspLysProLysGlnAlaGlnMetAsnGlnLysAspPhe       80
Db 404 TCTTCCCTGCCACCCCGAAGACAAGCCCCAACAGATGAATCAAAAGACTTT               463

Qy  81 LeuSerLeuIleValSerIleLeuArgSerTrpAsnGluTyrHisLeuValThr           100
Db 464 CTGAGCCTGATAGTCAGCATATTGCGATCCTGGAATGAGCCTCGTATCATCTGGTCACG      523

Qy 101 GluValArgGlyMetGlnGluAlaProGluAlaIleLeuSerLysSerAlaValGluIleGlu   120
Db 524 GAAGTACGTGGTATGCAAGAAGCCCCCAGAGGCTATCCTATCCAAAGGTGTAGAGATTGAG    583

Qy 121 GluGlnThrLysArgLeuGluGlyMetGluLeuValSerGlnValHisProGlu           140
Db 584 GAGCAAACCAAACGGCTTCTAGAGGGCATGAGCTGATAGTCACGCCAGGTTCATCCTGAA     643

Qy 141 ThrLysGluAsnGluIleTyrProValIleProSerGlyLeuProSerLeuGlnMetAlaAsp   160
Db 644 ACCAAAGAAAATGAGAATTACCCTGTCGTGGTCGGGACTTCATCCCTGCGGGACTTCATCCCTGAT 703

Qy 161 GluGluSerArgLeuSerArgAlaTyrTyrAsnLeuHisLeuHisCysLeuArgArgAspSerHis 180
Db 704 GAAGAGTCTCGCCTTTCTGCTTATTATAAACCTGCTCCACTGCCTACGCCAGGGATTCACAT    763

Qy 181 LysIleAspAsnTyrLeuLysLeuLysLysCysArgIleHisAsnAsnCys             199
Db 764 AAATCGACAAATTATCTCAAGCTCCTGAAGTGCCGAATCATCCACAACACAACTGC          820


RESULT 6
US-10-119-428-41
;  Sequence 41, Application US/1011 9428
;  Publication No. US20030165881A1
;  GENERAL INFORMATION:
;  APPLICANT: Tang, Y. Tom
;  APPLICANT: Liu, Chenghua
;  APPLICANT: Asundi, Vinod
;  APPLICANT: Xu, Chongjun
;  APPLICANT: Wehrman, Tom
;  APPLICANT: Ren, Peiyan
;  APPLICANT: Ma, Yunqing
;  APPLICANT: Zhou, Ping
;  APPLICANT: Zhao, Qing A.
;  A''PLICANT: Yang, Yonghong
;  APPLICANT: Drmanac, Radoje T.
;  TITLE OF INVENTION: No. US20030165881Alel Nucleic Acids and
;  TITLE OF INVENTION: Polypeptides
;  FILE REFERENCE: 789CIP2
;  CURRENT APPLICATION NUMBER: US/10/119,428
;  CURRENT FILING DATE: 2002-04-09
;  PRIOR APPLICATION NUMBER: 09/596,193
;  PRIOR FILING DATE: 2000-06-17
;  PRIOR APPLICATION NUMBER: 09/574,454
;  PRIOR FILING DATE: 2000-05-19
;  PRIOR APPLICATION NUMBER: 09/519,705
;  PRIOR FILING DATE: 2000-03-07
;  NUMBER OF SEQ ID NOS: 55
;  SOFTWARE: pt_FL_genes Version 1.0
;  SEQ ID NO 41
;  LENGTH: 1097
;  TYPE: DNA
;  ORGANISM: Homo sapiens
;  FEATURE:
;  NAME/KEY: CDS
;  LOCATION: (175)..(858)
;  FEATURE:
;  NAME/KEY: misc_feature
;  LOCATION: (1)...(1097)
;  OTHER INFORMATION: n = a,t,c or g
US-10-119-428-41

Alignment Scores:
Pred. No.:
Score:                    3.39e-129       Length:         1097
Percent Similarity:       1043.00         Matches:        199
Best Local Similarity:    100.00%         Conservative:   0
Query Match:              100.00%         Mismatches:     0
DB:                       15              Indels:         0
                                          Gaps:           0

US-10-735-594-1 (1-199) x US-10-119-428-41 (1-1097)

Qy   1 LeuProIleCysProGlyGlyValGlyAlaAlaArgCysGlnValThrLeuArgAspLeuPheAsp  20
Db 259 TTGCCCATCTGTCCGGCGGGGCTGCCGATGCCAGGTGACCCTTCGAGACCTGTTTGAC        318

Qy  21 ArgAlaValValLeuSerHisTyrIleHisAsnLeuSerGluMetPheSerGluPhe          40
Db 319 CGCGCCGTCGTCCTGTCCCACTACATCCATAACCTCTCCCAGAAATGTTCAGCGAATTC       378

Qy  41 AspLysArgGlyTyrThrHisGlyArgGlyPheIleThrLysAsnSerCysHisThr          60
Db 379 GATAAACGGTATACCCATGGCCGGGGGTTCATTACCAAGGCCATCAACAGCTGCCACACT      438

Qy  61 SerSerLeuAlaThrProGluAspLysProGlnAlaGlnMetAsnGlnLysAspPhe          80
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                    GenCore version 5.1.6
          Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:    September 13, 2004, 18:15:09 ; Search time 422 Seconds
                              (without alignments)
                      2003.297 Million cell updates/sec

Title:         US-10-735-594-1
Perfect score: 199
Sequence:      1 LPICPGGAARCQVTLRDLFD.........HKIDNYLKLLKCRIIHNNNC 199

Scoring table: OLIGO
           Xgapop  60.0 , Xgapext  60.0
           Ygapop  60.0 , Ygapext  60.0
           Fgapop   6.0 , Fgapext   7.0
           Delop    6.0 , Delext    7.0

Searched:    373863 seqs, 2124099041 residues

Word size:   1

Total number of hits satisfying chosen parameters:    6745146

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Command line parameters:
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-Q=/cgn_1/USPTO_spool_p/US10735594/runat_10092004_144725_5879/app_query.fasta_1.391
-DB=N Geneseq_29Jan04 -QFM=fastap -SUFFIX=olip2n.rng -MINMATCH=0.1 -LOOPCL=0
-LOOPEXT=0 -UNITS=bits -START=1 -END=-1 -MATRIX=oligo -TRANS=human40.cdi
-LIST=45 -DOCALIGN=200 -THR_SCORE=quality -THR_MIN=1 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
-USER=US10735594 @CGN_1_1_885 @runat_10092004_144725_5879 -NCPU=6 -ICPU=3
-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=60 -XGAPEXT=60 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=60 -YGAPEXT=60 -DELOP=6 -DELEXT=7
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      Pred. No. is the number of results predicted by chance to have a
      score greater than or equal to the score of the result being printed,
      and is derived by analysis of the total score distribution.

                              SUMMARIES

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Database : N_Geneseq_29Jan04:*
           1: geneseqn1980s:*
           2: geneseqn1990s:*
           3: geneseqn2000s:*
           4: geneseqn2001as:*
           5: geneseqn2001bs:*
           6: geneseqn2002s:*
           7: geneseqn2003as:*
           8: geneseqn2003bs:*
           9: geneseqn2003cs:*
          10: geneseqn2004s:*
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Result No.	Score	% Query Match	Length	DB	ID	Description
1	199	100.0	603	2	AAX01694	Aax01694 Human ant
2	199	100.0	833	6	ABV94102	Abv94102 Breast ca
3	199	100.0	960	2	AAQ03293	Aaq03293 Recombina
4	199	100.0	970	2	ACA56818	Aca56818 Signallin
5	199	100.0	1062	5	AAS44957	Aas44957 cDNA enco
6	199	100.0	1071	2	AAZ41975	Aaz41975 Human myo
7	199	100.0	1100	2	AAQ96139	Aaq96139 Prolactin
8	185	93.0	5278	2	AAQ05168	Aaq05168 Plasmid p

No.	c	Length	%	Score	Pred	ID	Description
9		181	91.0	3621	1	AAN60847	Aan60847 Human pre
10		143	71.9	889	7	AAL51963	Aal51963 Human ext
11	c	136	68.3	688	7	ABZ83636	Abz83636 Toxicolog
12		136	68.3	1066	2	AAL51964	Aal51964 Human ext
13		124	62.3	390	2	AAX58737	Aax58737 DNA encod
14		124	62.3	771	1	AAX58738	Aax58738 DNA encod
15		124	62.3	832	2	AAN80115	Aan80115 Human pre
16		123	61.8	375	2	AAV10505	Aav10505 Human pro
17		123	61.8	754	2	AAV10506	Aav10506 Human con
18		122	61.3	600	2	AAT74325	Aat74325 cDNA enco
19		81	40.7	423	2	AAX01696	Aax01696 Human ant
20		81	40.7	603	2	AAX01697	Aax01697 Human ant
21		76	38.2	818	2	AAL51960	Aal51960 Human ant
22		65	32.7	375	2	AAX01695	Aax01695 Human ant
23		63	31.7	309	3	AAC72604	Aac72604 Single nu
24		60	30.2	309	3	AAC72598	Aac72598 Single nu
25		59	29.6	282	3	AAC72601	Aac72601 Single nu
26		57	28.6	832	3	AAT74333	Aat74333 cDNA enco
27		48	24.1	282	3	AAC72595	Aac72595 Single nu
28		40	20.1	278	3	AAC72607	Aac72607 Single nu
29		20	10.1	60	6	ABN43525	Abn43525 Human spl
30		19	9.5	445	2	ABX39876	Abx39876 Bovine ES
31		19	9.5	600	2	AAT03456	Aat03456 Turkey pr
32		19	9.5	1281	2	AAT03457	Aat03457 Turkey pr
33		14	7.0	594	2	AAT74324	Aat74324 cDNA enco
34		14	7.0	822	1	AAN80114	Aan80114 Rat prepr
35		14	7.0	899	2	AAQ14451	Aaq14451 Rat prola
36	c	13	6.5	3735	2	AAQ14452	Aaq14452 Rat prola
37	c	13	6.5	48	6	ABS73117	Abs73117 Human gro
38		13	6.5	443	6	ABV94100	Abv94100 Breast ca
39		12	6.0	681	6	AAQ13553	Aaq13553 Prolactin
40		12	6.0	47	6	ABS73116	Abs73116 Human gro
41		12	6.0	47	9	ADE82299	Ade82299 XbaI-BstE
42		12	6.0	234	7	ABX41778	Abx41778 Bovine ES
43		12	6.0	292	7	ABX48868	Abx48868 Bovine ES
44		12	6.0	299	7	ABX44819	Abx44819 Bovine ES
45		12	6.0	312	7	ABX49800	Abx49800 Bovine ES

                                    ALIGNMENTS

```
RESULT 1
AAX01694
ID   AAX01694 standard; DNA; 603 BP.
XX
AC   AAX01694;
XX
DT   08-JUN-1999  (first entry)
XX
DE   Human anti-angiogenic hPRL Met-1Cys199 DNA.
XX
KW   Human; anti-angiogenic; prolactin; placental lactogen; hPL; angiogenesis;
KW   growth hormone; hGH; hGH-V; capillary endothelial cell proliferation;
KW   placental vascularisation; pregnancy; treatment; angiogenic disease;
KW   tumour; inhibitor; malignant; angiofibroma; arteriovenous malformation;
KW   arthritis; atherosclerotic plaques; corneal graft neovascularisation;
KW   wound healing; proliferative retinopathy; macular degeneration; trachoma;
KW   granulation; glaucoma; ocular; uveitis; fracture; Osler-Weber syndrome;
KW   psoriasis; fibroplasia; scleroderma; Kaposi's sarcoma; vascular adhesion;
KW   ulcer; leukaemia; reproductive disorder; contraceptive agent;
KW   gene therapy; pre-eclampsia; intrauterine growth retardation;
KW   placental dysfunction; ss.
XX
OS   Homo sapiens.
XX
PN   WO9851323-A1.
XX
PD   19-NOV-1998.
XX
PF   12-MAY-1998;  98WO-US009691.
XX
PR   13-MAY-1997;  97US-0046394P.
XX
```

```
Db  244 CTGAGCCTGATAGTCAGCATATTGCGATCCTCTGGAATGAGCCTCTGTATCATCTGGTCACG 303
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  101 GluValArgGlyMetGlnGluAlaProGluAlaIleLeuSerLysAlaValGluIleGlu   120

Db  304 GAAGTACCTGGTATGCAAGAAGCCCCGGAGGCTATCCTATCCAAAGCTGTAGAGATTGAG   363
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  121 GluGlnThrLysArgLeuLeuGlyMetGluValSerGlnValHisProGlu           140

Db  364 GAGCAAACCAAACGGCTTCTAGAGGGCATGAGGCTGATAGTCAGCCAGGTTCATCCTGAA   423
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  141 ThrLysGluAsnGluIleTyrProValTrpSerGlyLeuProSerLeuGlnMetAlaAsp  160

Db  424 ACCAAAGAAAATGAGATCTACCCTGTCTGGTCGGGACTTCCATCCCTGCAGATGGCTGAT   483
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  161 GluGluSerArgLeuSerAlaTyrfYrAsnLeuLeuHisCysLeuArgArgAspSerHis  180

Db  484 GAAGAGTCTCGCCTTCTGCTTATTATAACCTGCTCCCACTGGCTACGGCAGGGATTCACAT 543
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Qy  181 LysIleAspAsnTyrLeuLeuLysCysArgIleIleHisAsnAsnAsnCys           199

Db  544 AAAATCGACAATTATCTCAAGCTCCTGAAGTGCCGAATCATCCACAACAACACTGC      600
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RESULT 2
ABV94102
ID   ABV94102 standard; cDNA; 833 BP.
XX
AC   ABV94102;
XX
DT   08-JAN-2003 (first entry)
XX
DE   Breast carcinoma related nucleotide sequence SEQ ID NO:93.
XX
KW   Human; breast carcinoma; cancer; tumour; cytostatic; anti-tumour; gene;
KW   ss.
XX
OS   Homo sapiens.
XX
PN   WO20246467-A2.
XX
PD   13-JUN-2002.
XX
PF   07-DEC-2001; 2001WO-IB002811.
XX
PR   08-DEC-2000; 2000US-0254090P.
PR   07-DEC-2001; 2001US-00007926.
XX
PA   (IPSO-) IPSOGEN.
XX
PI   Bertucci F, Houlgatte R, Birnbaum D, Nguyen C, Viens P, Fert V;
XX
DR   WPI; 2002-619023/66.
XX
PT   Novel polynucleotide library useful in molecular characterization of a
PT   carcinoma, comprising a pool of polynucleotide sequences or its
PT   subsequences which are either underexpressed or overexpressed in tumor
PT   cells.
XX
PS   Claim 1; Page 172; 401pp; English.
XX
CC   The present invention describes a polynucleotide library (I) useful in
CC   the molecular characterisation of a carcinoma, comprising a pool of
CC   polynucleotides or its subsequences which are either underexpressed or
CC   overexpressed in tumour cells, and correspond to any of the
CC   polynucleotide sequences chosen from the 468 sequences given in ABV94010
CC   to ABV94477. Also described: (1) a polynucleotide array (II) useful for
CC   the prognosis or diagnostic of tumour, comprising (I); and (2) detecting
CC   (MI) differentially expressed polynucleotide sequences which are
CC   correlated with a cancer, involves obtaining a polynucleotide sample from
CC   a patient, and reacting the polynucleotide sample obtained with a probe
CC   immobilised on a solid support, where the probe comprises any combination
CC   of the polynucleotide sequences of (I) or its expression products encoded
CC   by polynucleotide sequences of (I), and detecting the reaction product.
CC   (I) have cytostatic activities and can be used as anti-tumour agents. (I)

PA   (REGC) UNIV CALIFORNIA.
XX
PI   Weiner RI, Martial JA, Struman I, Taylor R;
XX
DR   WPI; 1999-045192/04.
DR   P-PSDB; AAW92258.
XX
PT   New anti-angiogenic peptides - comprise N-terminal fragments of human
PT   placental lactogen, human growth hormone variant or human
PT   prolactin.
XX
PS   Example 3; Page 41; 87pp; English.
XX
CC   This invention describes novel human anti-angiogenic peptides derived
CC   from 10 to 150 consecutive amino acids selected from the N-terminal end
CC   of human placental lactogen (hPL), human growth hormone (hGH), growth
CC   hormone variant (hGH-V), or human prolactin. Such peptides (i) inhibit
CC   capillary endothelial cell proliferation and organisation (ii) inhibit
CC   angiogenesis in chick chorioallantoic membrane and (iii) binds to at
CC   least one specific receptor which does not bind an intact full length
CC   hGH, hPL, prolactin or hGH-V. The invention also describes a method for
CC   diagnosing a probable abnormality of placental vascularisation during
CC   pregnancy. The peptides can be used for treating an angiogenic disease in
CC   a subject, for inhibiting tumour formation or growth in a patient or for
CC   modulating vascularisation of a patient's placenta. In particular, the
CC   peptides can be used for preventing or treating e.g. malignant tumours,
CC   angiofibroma, arteriovenous malformation, arthritic such as rheumatoid
CC   arthritis, atherosclerotic plaques, corneal graft neovascularisation,
CC   delayed wound healing, proliferative retinopathy such as diabetic
CC   retinopathy, macular degeneration, granulations such as those occurring
CC   in haemophilic joints, inappropriate vascularisation in wound healing
CC   such as hypertrophic scars or keloid scars, neovascular glaucoma, ocular
CC   tumour, uveitis, non-union fractures, Osler-Weber syndrome, psoriasis,
CC   pyogenic glaucoma, retrolental fibroplasia, scleroderma, solid tumours,
CC   Kaposi's sarcoma, trachoma, vascular adhesions, chronic varicose ulcers,
CC   leukaemia, and reproductive disorders such as follicular and luteal cysts
CC   and choriocarcinoma. They can also be used as contraceptive agents. DNA
CC   encoding the peptides can be used in gene therapy. The measurement of
CC   abnormal levels of N-terminal fragments of hGH, hGH-V, prolactin or hPL
CC   can be used in assays for impairment of vascular development associated
CC   with pre-eclampsia, intrauterine growth retardation, and placental
CC   dysfunction
XX
SQ   Sequence 603 BP; 161 A; 173 C; 134 G; 135 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.:   4.3e-192
Score: 199.00   Length: 603
Percent Similarity: 100.00%   Matches: 199
Best Local Similarity: 100.00%   Conservative: 0
Query Match: 100.00%   Mismatches: 0
DB: 2   Indels: 0
                                               Gaps: 0

US-10-735-594-1 (1-199) x AAX01694 (1-603)

```
Qy    1 LeuProIleCysProGlyGlyValAlaAlaArgCysGlnValThrLeuArgAspLeuPheAsp  20
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    4 TTGCCCATCTGTCCCGGCGGCGGGGCTGCCGATGCCAGGTGCACCCTGCGAGACCTGTTTGAC  63

Qy   21 ArgAlaValValLeuSerHisTyrIleHisAsnLeuSerSerGluMetPheSerGluPhe    40
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   64 CGGGCCGTGGTCCTGTCCCACTACATCCCACATAACCTCTCCTCCAGAAATGTTCAGCGAATTC 123

Qy   41 AspLysArgTyrThrHisGlyAlaArgGlyPheIleThrLysAlaIleAsnSerCysHisThr  60
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  124 GATAAACGGTATACCCATGGCGCGGGGGTTCATTACCAAGGCCATCAACAGCTGCCACACT   183

Qy   61 SerSerLeuAlaThrProGluAspLysGluGlnIleAlaGlnMetAsnGlnLysAspPhe    80
        |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  184 TCTTCCCTTGCACCCCGAGACAAGGAGCAAGCCCAACAGATGAATCAAAAAGACTTT     243

Qy   81 LeuSerLeuIleValSerIleLeuArgSerTrpAsnGluProLeuTyrHisLeuValThr   100
        ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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```
                    GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:     September 13, 2004, 12:06:10 ; Search time 40 Seconds
                                          (without alignments)
                            478.553 Million cell updates/sec

Title:      US-10-735-594-1
Perfect score: 1043
Sequence:   1 LPICPGGAARCQVTLRDLFD.........HKIDNVLKLLKCRIIHNNNC 199

Scoring table: BLOSUM62
            Gapop 10.0 , Gapext 0.5

Searched:   283366 seqs, 96191526 residues

Total number of hits satisfying chosen parameters:    283366

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :  PIR_78:*
            1: pir1:*
            2: pir2:*
            3: pir3:*
            4: pir4:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                            SUMMARIES
```

Result No.	Score	% Match	Query Length	DB	ID	Description
1	1043	100.0	227	1	LCHU	prolactin precurso
2	1031	98.8	228	2	A61402	prolactin precurso
3	887	85.0	199	2	S15131	prolactin - Arabia
4	877	84.1	229	1	LCPG	prolactin precurso
5	876	84.0	199	1	LCHO	prolactin - horse
6	867	83.1	229	2	JC4631	prolactin precurso
7	861	82.6	199	2	PN0128	prolactin - sei wh
8	797	76.4	229	1	LCBO	prolactin precurso
9	796	76.3	229	1	LCSH	prolactin precurso
10	796	76.3	229	2	I83982	prolactin - goat
11	790.5	75.8	198	1	A60620	prolactin - green
12	772	74.0	175	2	S18882	prolactin - Americ
13	770	73.8	229	2	A60972	prolactin precurso
14	754	72.3	229	2	A61133	prolactin precurso
15	737	70.7	199	2	JS0430	prolactin - elepha
16	690.5	66.2	207	2	A60969	prolactin precurso
17	667	64.0	226	1	LCRT	prolactin - golden
18	657	63.0	226	2	A49159	prolactin precurso
19	621	59.5	228	1	LCMS	prolactin precurso
20	601.5	57.7	200	2	S34604	prolactin - marble
21	494	47.4	134	2	I51233	prolactin - Japane
22	468	44.9	236	2	A37930	placental lactogen
23	464.5	44.5	221	2	A41407	placental lactogen
24	443	42.5	236	2	A40143	placental lactogen
25	417.5	40.0	222	2	A26489	placental lactogen
26	416.5	39.9	238	2	B36284	prolactin-like pro
27	415.5	39.8	267	2	A34078	prolactin-related
28	402.5	38.6	221	2	A25951	placental lactogen
29	387	37.1	238	2	A31417	prolactin-related
30	370.5	35.5	223	2	A49160	placental lactogen
31	367	35.2	224	2	A40062	lactogen I precurs
32	362	34.7	234	2	A40919	prolactin-like pro
33	361	34.6	239	2	S04966	prolactin-like pro
34	360	34.5	237	2	S14722	hypothetical prote
35	358.5	34.4	244	2	A22722	proliferin-related
36	350	33.6	213	2	B34078	prolactin-related
37	340.5	32.6	230	2	A37399	lactogen I precurs
38	316.5	30.3	227	2	A24911	prolactin-like pro
39	316	30.3	224	2	S48671	proliferin - human
40	316	30.3	224	2	A05086	proliferin 1 precu
41	315	30.2	224	2	S05648	proliferin 3 - mou
42	312	29.9	209	2	S30541	prolactin precurso
43	310.5	29.8	212	2	I51275	prolactin precurso
44	310	29.7	224	2	A23159	proliferin 2 precu
45	287	27.5	210	2	S34351	prolactin precurso

```
                            ALIGNMENTS

RESULT 1
LCHU
prolactin precursor [validated] - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1979 #sequence_revision 23-Oct-1981 #text_change 08-Dec-2000
C;Accession: A90998; A92318; A28867; PN0089; A92762; A92177; A01505
R;Truong, A.T.; Duez, C.; Belayew, A.; Renard, A.; Pictet, R.; Bell, G.I.; Martial, J.A.
EMBO J. 3, 429-437, 1984
A;Title: Isolation and characterization of the human prolactin gene.
A;Reference number: A90998; MUID:84182507; PMID:6325171
A;Accession: A90998
A;Molecule type: DNA
A;Residues: 1-227 <TRU>
R;Cooke, N.E.; Coit, D.; Shine, J.; Baxter, J.D.; Martial, J.A.
J. Biol. Chem. 256, 4007-4016, 1981
A;Title: Human prolactin: cDNA structural analysis and evolutionary comparisons.
A;Reference number: A92318; MUID:81168179; PMID:6260780
A;Accession: A92318
A;Molecule type: mRNA
A;Residues: 1-227 <COO>
A;Cross-references: GB:V00566; GB:V00299; GB:J00299; NID:g34210; PIDN:CAA23829.1; PID:g34211
R;Takahashi, H.; Nabeshima, Y.; Nabeshima, Y.; Ogata, K.; Takeuchi, S.
J. Biochem. 95, 1491-1499, 1984
A;Title: Molecular cloning and nucleotide sequence of DNA complementary to human decidua
A;Reference number: A28867; MUID:84264464; PMID:6146607
A;Accession: A28867
A;Molecule type: mRNA
A;Residues: 1-205,'H',207-227 <TAK>
A;Cross-references: EMBL:M29386
A;Note: the authors translated the codon CAT for residue 206 as Asp
R;Mertvetsov, N.P.; Golovin, S.Y.; Zelenin, S.M.; Morozova, T.V.; Karginov, V.A.; Chekhu
Bioorg. Khim. 13, 1687-1690, 1987
A;Title: Synthesis, cloning and sequencing of cDNA complementary to mRNA of prolactin fr
A;Reference number: PN0089; MUID:88221681; PMID:3450284
A;Accession: PN0089
A;Molecule type: mRNA
A;Residues: 45-227 <MER>
A;Experimental source: pituitary gland
A;Note: the authors translated the codon AAC for residue 15 as Asp
R;Shome, B.; Parlow, A.F.
J. Clin. Endocrinol. Metab. 45, 1112-1115, 1977
A;Title: Human pituitary prolactin (hPRL): the entire linear amino acid sequence.
A;Reference number: A92762; MUID:78046207; PMID:925136
A;Accession: A92762
A;Molecule type: protein
A;Residues: 29-109,'VS',112,'L','L';115-132,'X',134-171,'D',173-189,'SE',192-227 <SHO>
R;Jacobs, J.W.; Niall, H.D.
J. Biol. Chem. 250, 3629-3636, 1975
A;Title: High sensitivity automated sequence determination of polypeptides.
A;Reference number: A92177; MUID:75151509; PMID:1126929
A;Accession: A92177
A;Molecule type: protein
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A;Residues: 29-52,'L' <JAC>
C;Genetics:
A;Gene: GDB:PRL
A;Cross-references: GDB:119517; OMIM:176760
A;Map position: 6p22.2-6p22.1
A;Introns: 9/3; 68/3; 104/3; 164/3
C;Superfamily: prolactin
C;Keywords: anterior pituitary; hormone; lactation; placenta
F;1-28/Domain: signal sequence #status predicted <SIG>
F;29-227/Product: prolactin #status experimental <MAT>
F;32-39,86-202,219-227/Disulfide bonds: #status predicted

Query Match   100.0%;   Score 1043;   DB 1;   Length 227;
Best Local Similarity   100.0%;   Pred. No. 3.8e-78;
Matches   199;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

Qy   1 LPICPGGAARCQVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFITKAINSCHT 60
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   29 LPICPGGAARCQVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFITKAINSCHT 88

Qy   61 SSLATPEDKEQAQQMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   89 SSLATPEDKEQAQQMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 148

Qy   121 EQTKRLLEGMELIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSH 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   149 EQTKRLLEGMELIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSH 208

Qy   181 KIDNYLKLLKCRIIHNNNC 199
           |||||||||||||||||||
Db   209 KIDNYLKLLKCRIIHNNNC 227

RESULT 2
A61402
prolactin precursor, placental (clone 204) - human
C;Species: Homo sapiens (man)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 16-Feb-1997
C;Accession: A61402
R;Hiraoka, Y.; Tatsumi, K.; Shiozawa, M.; Aiso, S.; Fukasawa, T.; Yasuda, K.; Miyai, K.
Mol. Cell. Endocrinol. 75, 71-80, 1991
A;Title: A placenta-specific 5' non-coding exon of human prolactin.
A;Reference number: A61402; MUID:91267286; PMID:2050267
A;Accession: A61402
A;Status: preliminary; not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-228 <HIR>
C;Superfamily: prolactin
C;Keywords: alternative splicing
F;87-203,220-228/Disulfide bonds: #status predicted

Query Match   98.8%;   Score 1031;   DB 2;   Length 228;
Best Local Similarity   99.5%;   Pred. No. 3.7e-77;
Matches   198;   Conservative   0;   Mismatches   1;   Indels   0;   Gaps   0;

Qy   1 LPICPGGAARCQVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFITKAINSCHT 60
           ||||| |||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   30 LPIKPGGAARCQVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFITKAINSCHT 89

Qy   61 SSLATPEDKEQAQQMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   90 SSLATPEDKEQAQQMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 149

Qy   121 EQTKRLLEGMELIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSH 180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   150 EQTKRLLEGMELIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSH 209

Qy   181 KIDNYLKLLKCRIIHNNNC 199
           |||||||||||||||||||
Db   210 KIDNYLKLLKCRIIHNNNC 228

RESULT 3

S15131
prolactin - Arabian camel
C;Species: Camelus dromedarius (Arabian camel)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 11-May-2000
C;Accession: S15131; A60513
R;Martinat, N.; Huet, J.C.; Nespoulous, C.; Combarnous, Y.; Pernollet, J.C.
Biochim. Biophys. Acta 1077, 339-345, 1991
A;Title: Determination of the primary and secondary structures of the dromedary (Camelus
A;Reference number: S15131; MUID:91230144; PMID:2029533
A;Accession: S15131
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-199 <MAR>
R;Martinat, N.; Anouassi, A.; Huet, J.C.; Pernollet, J.C.; Combarnous, Y.
Comp. Biochem. Physiol. B 97, 667-674, 1990
A;Title: Purification and characterization of glycosylated and non-glycosylated forms of
A;Reference number: A60513; MUID:91199560; PMID:2085952
A;Accession: A60513
A;Molecule type: protein
A;Residues: 1-40 <MA2>
C;Superfamily: prolactin
C;Keywords: anterior pituitary; hormone; lactation; placenta

Query Match   85.0%;   Score 887;   DB 2;   Length 199;
Best Local Similarity   81.4%;   Pred. No. 1.9e-65;
Matches   162;   Conservative   22;   Mismatches   15;   Indels   0;   Gaps   0;

Qy   1 LPICPGGAARCQVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFITKAINSCHT 60
           |||| || ||||| |||||||||||||||||||||||||||||| ||||||||||||||
Db   1 LPICPSGAVNCQVSLRDLFDRAVVLSHYIHNLSSEMFNEFDKRYAQGRGFMTKAINSCHT 60

Qy   61 SSLATPEDKEQAQQMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 120
           |||:||||||||||| | :|:|: |||| |||:| :::::||||||||| |||:::|:|
Db   61 SSLSTPEDKEQAQQIHHEDLLNLVLRVLRSWNDPLYHLVTEVRGMQEAPDAILSRAIEIE 120

Qy   121 EQTKRLLEGMELIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSH 180
           |||:||||||||| |||||: :::|:||||||||||||||||:||||:::||||||||||
Db   121 EQNKRLLEGMEKIVGQVHPGVKENEIYSVWSGLPSLQMADEDTRLFAFYNLLHCLRRDSH 180

Qy   181 KIDNYLKLLKCRIIHNNNC 199
           ||||||||||||||:::|
Db   181 KIDNYLKLLKCRIIYDSNC 199

RESULT 4
LCPG
prolactin precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Apr-1984 #sequence_revision 27-Jun-1994 #text_change 18-Jun-1999
C;Accession: S04077; A60971; A01507
R;Schulz-Aellen, M.F.; Schmid, E.; Movva, R.N.
Nucleic Acids Res. 17, 3295, 1989
A;Title: Nucleotide sequence of porcine preprolactin cDNA.
A;Reference number: S04077; MUID:89263739; PMID:2726463
A;Accession: S04077
A;Molecule type: mRNA
A;Residues: 1-229 <SCH>
A;Cross-references: EMBL:X14068; NID:g2082; PIDN:CAA32231.1; PID:g2083
R;Kato, Y.; Hirai, T.; Kato, T.
J. Mol. Endocrinol. 4, 135-142, 1990
A;Title: Molecular cloning of cDNA for porcine prolactin precursor.
A;Reference number: A60971; MUID:90262633; PMID:2344390
A;Accession: A60971
A;Molecule type: mRNA
A;Residues: 1-3,'R',5,'X',7-42,'V',44-229 <KAT>
R;Li, C.H.
Int. J. Pept. Protein Res. 8, 205-224, 1976
A;Title: Studies on pituitary lactogenic hormone. The primary structure of the porcine
A;Reference number: A91770; MUID:76189476; PMID:1270193
A;Accession: A01507
A;Molecule type: protein
A;Residues: 31-42,'V',44-151,'E',153-225,'N',227-229 <LIC>
C;Superfamily: prolactin

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                    GenCore version 5.1.6
              Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:      September 13, 2004, 11:39:59 ; Search time 24 seconds
                                            (without alignments)
                                            431.748 Million cell updates/sec

Title:       US-10-735-594-1
Perfect score: 1043
Sequence:    1 LPICPGGAARCQVTLRDLFD.........HKIDNYLKLLKCRIIHNNNC 199

Scoring table: BLOSUM62
             Gapop 10.0 , Gapext 0.5

Searched:    141681 seqs, 52070155 residues

Total number of hits satisfying chosen parameters:        141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                    SUMMARIES

                %
Result       Query
No.   Score  Match Length DB ID           Description
----  -----  ----- ------ -- --           -----------
  1   1043   100.0   227  1  PRL_HUMAN     P01236 homo sapien
  2   1029    98.7   227  1  PRL_MACMU     P55151 macaca mula
  3    887    85.0   199  1  PRL_CAMDR     P22393 camelus dro
  4    880    84.4   229  1  PRL_PIG       P01238 sus scrofa
  5    876    84.0   199  1  PRL_HORSE     P12420 equus cabal
  6    874    83.8   227  1  PRL_RABIT     Q28632 oryctolagus
  7    867    83.1   229  1  PRL_FELCA     P46403 felis silve
  8    861    82.6   199  1  PRL_BALBO     P33089 balaenopter
  9    857    82.2   228  1  PRL_TRIVU     O62781 trichosurus
 10    852    81.7   193  1  PRL_MUSVI     P29234 mustela vis
 11    847    81.2   228  1  PRL_MONDO     O62819 monodelphis
 12    798    76.5   229  1  PRL_CAPHI     Q28318 capra hircu
 13    797    76.4   229  1  PRL_BOVIN     P01239 bos taurus
 14    796    76.3   229  1  PRL_SHEEP     P01240 ovis aries
 15  790.5    75.8   198  1  PRL_CHEMY     P33090 chelonia my
 16    777    74.5   199  1  PRL2_ALLMI    P55752 alligator m
 17    776    74.4   199  1  PRL2_CRONO    P55754 crocodylus
 18    772    74.0   199  1  PRL1_ALLMI    P55751 alligator m
 19    771    73.9   199  1  PRL1_CRONO    P55753 crocodylus
 20    770    73.8   229  1  PRL_CHICK     P14676 gallus gall
 21    754    72.3   229  1  PRL_MELGA     P17572 meleagris g
 22    737    70.7   199  1  PRL_LOXAF     P10765 loxodonta a
 23    667    64.0   226  1  PRL_RAT       P01237 rattus norv
 24    657    63.0   226  1  PRL_MESAU     P37884 mesocricetu
 25    621    59.5   226  1  PRL_MOUSE     P06879 mus musculu
 26  609.5    58.4   200  1  PRL_PROAT     P33091 protopterus
 27    494    47.4   134  1  PRL_BUFJA     P43001 bufo japoni
 28    470    45.1   236  1  PLL1_BOVIN    P09611 bos taurus
 29  464.5    44.5   221  1  PLL2_MESAU    P14059 mesocricetu
 30    443    42.5   236  1  PLL_SHEEP     P16038 ovis aries
 31  417.5    40.0   222  1  PLL2_MOUSE    P09586 mus musculu
 32  416.5    39.9   238  1  PLL2_BOVIN    P19159 bos taurus
 33  415.5    39.8   267  1  PRR2_BOVIN    P12401 bos taurus
```

```
 34    402.5   38.6   221  1  PLL2_RAT    P09321 rattus norv
 35    379     36.3   238  1  PRR1_BOVIN  P05402 bos taurus
 36    368.5   35.3   244  1  PLFR_MOUSE  P04769 mus musculu
 37    367     35.2   224  1  PLL1_MOUSE  P18121 mus musculu
 38    364     34.9   223  1  PLLV_RAT    P34207 rattus norv
 39    362     34.7   234  1  PRRB_RAT    P24800 rattus norv
 40    361     34.6   239  1  PRR4_BOVIN  P18917 bos taurus
 41    350     33.6   213  1  PRR3_BOVIN  P12402 bos taurus
 42    340.5   32.6   230  1  PLL1_RAT    P21702 rattus norv
 43    316.5   30.3   227  1  PRRA_RAT    P09320 rattus norv
 44    316     30.3   224  1  PLF1_MOUSE  P04095 mus musculu
 45    315     30.2   224  1  PLF3_MOUSE  P18918 mus musculu
```

                              ALIGNMENTS

```
RESULT 1
PRL_HUMAN
ID   PRL_HUMAN      STANDARD;      PRT;    227 AA.
AC   P01236; Q15199; Q92996;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Prolactin precursor (PRL).
GN   PRL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=84182507; PubMed=6325171;
RA   Truong A.T., Duez C., Belayew A., Renard A., Pictet R.L., Bell G.I.,
RA   Martial J.A.;
RT   "Isolation and characterization of the human prolactin gene.";
RL   EMBO J. 3:429-437(1984).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=81168179; PubMed=6260780;
RA   Cooke N.E., Coit D., Shine J., Baxter J.D., Martial J.A.;
RT   "Human prolactin. cDNA structural analysis and evolutionary
RT   comparisons.";
RL   J. Biol. Chem. 256:4007-4016(1981).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=91267286; PubMed=2050267;
RA   Hiraoka Y., Tatsumi K., Shiozawa M., Aiso S., Fukasawa T., Yasuda K.,
RA   Miyai K.;
RT   "A placenta-specific 5'non-coding exon of human prolactin.";
RL   Mol. Cell. Endocrinol. 75:71-80(1990).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
```

```
FT   DISULFID      32     39       BY SIMILARITY.
FT   DISULFID      86    202       BY SIMILARITY.
FT   DISULFID     219    227       BY SIMILARITY.
FT   CARBOHYD      59     59       N-LINKED (GLCNAC...).
FT   CONFLICT      42     42       T -> A (IN REF. 6).
FT   CONFLICT     110    111       SL -> VS (IN REF. 7).
FT   CONFLICT     113    114       VS -> L (IN REF. 7).
FT   CONFLICT     118    118       S -> P (IN REF. 6).
FT   CONFLICT     148    148       E -> Q (IN REF. 5).
FT   CONFLICT     172    172       N -> D (IN REF. 7).
FT   CONFLICT     190    191       ES -> SE (IN REF. 7).
FT   CONFLICT     206    206       D -> H (IN REF. 5).
SQ   SEQUENCE     227 AA;   25876 MW;  952BBA1B6A955527 CRC64;

Query Match             100.0%;  Score 1043;  DB 1;  Length 227;
Best Local Similarity   100.0%;  Pred. No. 7.6e-77;
Matches  199;  Conservative    0;  Mismatches   0;  Indels   0;  Gaps   0;

Qy    1  LPICPGGAARCQVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFITKAINSCHT   60
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Db   29  LPICPGGAARCQVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFITKAINSCHT   88

Qy   61  SSLATPEDKEQAQQMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE  120
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   89  SSLATPEDKEQAQQMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE  148

Qy  121  EQTKRLLEGMELIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSH  180
         ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  149  EQTKRLLEGMELIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSH  208

Qy  181  KIDNYLKLKCRIIHNNNC  199
         ||||||||||||||||||
Db  209  KIDNYLKLKCRIIHNNNC  227

RESULT 2
PRL_MACMU
ID   PRL_MACMU     STANDARD;      PRT;    227 AA.
AC   P55151;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Prolactin precursor (PRL).
GN   PRL.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Decidua;
RX   MEDLINE=94220570; PubMed=8167226;
RA   Brown N.A., Bethea C.L.;
RT   "Cloning of decidual prolactin from rhesus macaque.";
RL   Biol. Reprod. 50:543-552(1994).
CC   -!- FUNCTION: Prolactin acts primarily on the mammary gland by
CC       promoting lactation.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the somatotropin/prolactin family.
CC   ---------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; U09018; AAA18471.1; -.
DR   HSSP; Q28632; 1AN3.
DR   InterPro; IPR001400; Somatotropin.
DR   Pfam; PF00103; hormone; 1.
```

```
RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   SEQUENCE OF 11-227 FROM N.A.
RX   MEDLINE=84264464; PubMed=6146607;
RA   Takahashi H., Nabeshima Y., Ogata K., Takeuchi S.;
RT   "Molecular cloning and nucleotide sequence of DNA complementary to
RT   human decidual prolactin mRNA.";
RL   J. Biochem. 95:1491-1499(1984).
RN   [6]
RP   SEQUENCE OF 11-201 FROM N.A.
RC   TISSUE=Breast;
RX   MEDLINE=97411082; PubMed=9266104;
RA   Shaw-Bruha C.M., Pirrucello S.J., Shull J.D.;
RT   "Expression of the prolactin gene in normal and neoplastic human
RT   breast tissues and human mammary cell lines: promoter usage and
RT   alternative mRNA splicing.";
RL   Breast Cancer Res. Treat. 44:243-253(1997).
RN   [7]
RP   SEQUENCE OF 29-227.
RX   MEDLINE=78046207; PubMed=925136;
RA   Shome B., Parlow A.F.;
RT   "Human pituitary prolactin (hPRL): the entire linear amino acid
RT   sequence.";
RL   J. Clin. Endocrinol. Metab. 45:1112-1115(1977).
RN   [8]
RP   SEQUENCE OF 29-53.
RX   MEDLINE=76151509; PubMed=1126929;
RA   Jacobs J.W., Niall H.D.;
RT   "High sensitivity automated sequence determination of polypeptides.";
RL   J. Biol. Chem. 250:3629-3636(1975).
CC   -!- FUNCTION: Prolactin acts primarily on the mammary gland by
CC       promoting lactation.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the somatotropin/prolactin family.
CC   -!- CAUTION: Ref.3 sequence differs from that shown due to a
CC       frameshift in position 8.
CC   ---------------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   ---------------------------------------------------------------------------
DR   EMBL; X00540; CAA25214.1; -; JOINED.
DR   EMBL; X00541; CAA25214.1; -; JOINED.
DR   EMBL; X00543; CAA25214.1; -; JOINED.
DR   EMBL; X00544; CAA25214.1; -; JOINED.
DR   EMBL; V00566; CAA23829.1; -; -.
DR   EMBL; X54393; CAA38263.1; -; ALT_FRAME.
DR   EMBL; X54393; CAA38264.1; -; ALT_FRAME.
DR   EMBL; BC015850; AAH15850.1; -; -.
DR   EMBL; M29386; AAA60173.1; -; -.
DR   EMBL; D00411; BAA00312.1; -; -.
DR   EMBL; U75583; AAB70858.1; -; -.
DR   PIR; A90998; LCHU.
DR   HSSP; Q28632; 1AN3.
DR   Genew; HGNC:9445; PRL.
DR   MIM; 176760; -.
DR   GO; GO:0005148; F:prolactin receptor binding; TAS.
DR   GO; GO:0008283; P:cell proliferation; TAS.
DR   GO; GO:0007166; P:cell surface receptor linked signal transdu...; TAS.
DR   GO; GO:0007516; P:hemocyte development; TAS.
DR   InterPro; IPR001400; Somatotropin.
DR   Pfam; PF00103; hormone; 1.
DR   PRINTS; PR00836; SOMATOTROPIN.
DR   PROSITE; PS00266; SOMATOTROPIN_1; 1.
DR   PROSITE; PS00338; SOMATOTROPIN_2; 1.
KW   Hormone; Lactation; Pituitary; Signal; Glycoprotein.
FT   SIGNAL        1     28
FT   CHAIN        29    227       PROLACTIN.
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            GenCore version 5.1.6
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```

OM protein - protein search, using sw model

Run on: September 13, 2004, 12:01:35 ; Search time 116 Seconds
                                             (without alignments)
                                             541.277 Million cell updates/sec

Title: US-10-735-594-1
Perfect score: 1043
Sequence: 1 LPICPGGAARCQVTLRDLFD.........HKIDNYLKLLKCRIIHNNNC 199

Scoring table: BLOSUM62
                 Gapop 10.0 , Gapext 0.5

Searched: 1017041 segs, 315518202 residues

Total number of hits satisfying chosen parameters: 1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Database :   SPTREMBL_25:*
                  1: sp_archea:*
                  2: sp_bacteria:*
                  3: sp_fungi:*
                  4: sp_human:*
                  5: sp_invertebrate:*
                  6: sp_mammal:*
                  7: sp_mhc:*
                  8: sp_organelle:*
                  9: sp_phage:*
                 10: sp_plant:*
                 11: sp_rodent:*
                 12: sp_virus:*
                 13: sp_vertebrate:*
                 14: sp_unclassified:*
                 15: sp_rvirus:*
                 16: sp_bacteriap:*
                 17: sp_archeap:*

SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1014	97.2	199	6	Q9TS41	Q9ts41 papio (babo
2	878	84.2	229	6	Q8HXS1	Q8hxs1 ailuropoda
3	877	84.1	229	6	Q864R8	Q864r8 mustela vis
4	838	80.3	222	5	Q8T1I0	Q8t1i0 taenia hyda
5	752	72.1	233	13	Q7T1A5	Q7t1a5 ambystoma b
6	748	71.7	229	13	Q90ZB1	Q90zb1 gallus gall
7	690.5	66.2	214	13	Q8JFX6	Q8jfx6 rana catesb
8	659	63.2	225	11	Q9QZL1	Q9qzl1 microtus mo
9	621	59.5	225	11	Q9CPQ0	Q9cpq0 mus musculu
10	621	59.5	225	11	Q9CYL2	Q9cyl2 mus musculu
11	621	59.5	226	11	Q9CYL8	Q9cyl8 mus musculu
12	621	59.5	228	11	Q9CPQ2	Q9cpq2 mus musculu
13	464	44.5	161	11	Q63293	Q63293 rattus norv
14	446	42.8	236	6	O77687	o77687 ovis aries
15	430.5	41.3	227	11	Q8K3W4	Q8k3w4 rattus norv
16	425.5	40.8	227	11	Q9CQR8	Q9cqr8 mus musculu
17	421.5	40.4	251	11	Q8CJ42	Q8CJ42 rattus norv
18	416	39.9	228	11	Q9JHK0	Q9JHK0 mus musculu
19	415	39.8	228	11	Q9JI05	Q9JI05 mus musculu
20	409.5	39.3	251	11	Q9DAX1	Q9DAX1 mus musculu
21	403	38.6	230	11	O35257	O35257 mus musculu
22	402.5	38.6	251	11	Q8CGZ9	Q8CGZ9 mus musculu
23	400.5	38.4	251	11	Q9CRB5	Q9CRB5 mus musculu
24	377	36.1	228	11	Q9JII3	Q9JII3 rattus norv
25	376.5	36.1	229	11	Q63435	Q63435 rattus norv
26	373	35.8	223	11	Q8CGZ7	Q8CGZ7 mus musculu
27	371	35.6	223	11	Q8BNL4	Q8BNL4 mus musculu
28	369	35.4	223	11	Q8CGZ6	Q8CGZ6 mus musculu
29	368.5	35.3	243	11	Q9DAY8	Q9DAY8 mus musculu
30	368	35.3	223	11	Q8CGZ8	Q8CGZ8 mus musculu
31	362.5	34.8	245	11	Q9R005	Q9R005 rattus norv
32	360	34.5	237	6	Q28135	Q28135 bos taurus
33	358.5	34.4	227	11	O35256	O35256 mus musculu
34	358.5	34.4	244	11	P70231	P70231 mus musculu
35	355	34.0	156	6	O97752	O97752 bos taurus
36	349	33.5	228	11	Q9JKL9	Q9JKL9 rattus norv
37	345	33.1	228	11	Q9R0R8	Q9R0R8 rattus norv
38	344	33.0	220	11	Q9R0S8	Q9R0S8 rattus norv
39	334.5	32.1	227	11	Q9JII4	Q9JII4 rattus norv
40	323	31.0	228	11	Q9DAZ2	Q9DAZ2 mus musculu
41	322	30.9	222	11	Q9JLV9	Q9JLV9 mus musculu
42	318.5	30.5	230	11	Q9JII2	Q9JII2 mus musculu
43	316.5	30.3	230	11	Q80X20	Q80X20 mus musculu
44	316	30.3	224	11	Q7TND2	Q7TND2 mus musculu
45	311	29.8	209	13	Q7ZZV3	Q7ZZV3 anguilla ja

ALIGNMENTS

RESULT 1
Q9TS41
ID   Q9TS41   PRELIMINARY;   PRT;   199 AA.
AC   Q9TS41;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Prolactin.
OS   Papio (baboons).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae;
OX   NCBI_TaxID=9554;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92037387; PubMed=1935793;
RA   Cole E.S., Nichols E.H., Lauziere K., Edmunds T., McPherson J.M.;
RT   "Characterization of the microheterogeneity of recombinant primate
RT   prolactin: implications for posttranslational modifications of the
RT   hormone in vivo.";
RL   Endocrinology 129:2639-2646(1991).
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
DR   InterPro; IPR001400; Somatotropin.
DR   Pfam; PF00103; hormone; 1.
DR   PRINTS; PR00836; SOMATOTROPIN.
DR   PROSITE; PS00266; SOMATOTROPIN_1; 1.
DR   PROSITE; PS00338; SOMATOTROPIN_2; 1.
SQ   SEQUENCE 199 AA; 22850 MW; 872A8935FEA43B67 CRC64;

Query Match   97.2%; Score 1014; DB 6; Length 199;
Best Local Similarity   96.5%; Pred. No. 9.9e-82;
Matches 192; Conservative   5; Mismatches   2; Indels   0; Gaps   0;

Qy   1 LPICPGGAARCQVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFITKAINSCHT 60
             ||||||||||||||||||||||||||||||||||||||||||:||||||||||:||||||
Db   1 LPICPGGAARCQVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKQYTHGRGFITRAINSCHT 60

Qy   61 SSLATPEDKEQAQQMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 120

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Db         |||    ||||:::||||||||||||||||||||||||||||||||||||||
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Qy       121 EQTKRLLEGMELIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSH 180
             |||||||||||||||||||||:||||||||||||
Db       121 EQTKRLLEGMELIVSQVHPETKENEIYPVWTGLPSLGMADEESRLSAYYNLLHCLRRDSH 180

Qy       181 KIDNYLKLLKCRIIHNNNC 199
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Db       181 KIDNYLKLLKCRIIHNNNC 199

RESULT 2
Q8HXS1
ID   Q8HXS1        PRELIMINARY;       PRT;   229 AA.
AC   Q8HXS1;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Prolactin precursor.
OS   Ailuropoda melanoleuca (Giant panda).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ailuropoda.
OX   NCBI_TaxID=9646;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pituitary;
RA   Zheng X., Zhu M., Zhang Z.;
RT   "Cloning and expression of pituitary prolactin gene in Ailuropoda
RT   melanoleuca.";
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY161285; AAN78320.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
DR   InterPro; IPR001400; Somatotropin.
DR   Pfam; PF00103; hormone_1.
DR   PRINTS; PR00836; SOMATOTROPIN.
DR   PROSITE; PS00266; SOMATOTROPIN_1; 1.
DR   PROSITE; PS00338; SOMATOTROPIN_2; 1.
KW   Signal.
FT   SIGNAL        1     30       POTENTIAL.
SQ   SEQUENCE   229 AA;  26236 MW;  441E3D748CFDDBC2 CRC64;

Query Match             84.2%;  Score 878;  DB 6;  Length 229;
Best Local Similarity   79.9%;  Pred. No. 1.3e-69;
Matches  159;  Conservative   25;  Mismatches   15;  Indels    0;  Gaps    0;

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             ||||||  |:  ||:||||||||||||||||||||:||:||||  |||||||||||||||
Db        31 LPICPTGAVNCQVSLRDLFDRAVILSHYIHNLSSEMFNEFDKRYAQGRGFITKAINSCHT 90

Qy        61 SSLATPEDKEQAQQMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 120
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Qy       121 EQTKRLLEGMELIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSH 180
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Db       151 EQNRRLLEGMEKIVGQVHPGVRENEVYSVWSGLPSLQMADEDTRLFAFYNLLHCLRRDSH 210

Qy       181 KIDNYLKLLKCRIIHNNNC 199
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Db       211 KIDNYLKLLKCRIVYDSNC 229

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Q864R8
ID   Q864R8        PRELIMINARY;       PRT;   229 AA.
AC   Q864R8;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Preprolactin precursor.
OS   Mustela vison (American mink).
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OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC   Mustela.
OX   NCBI_TaxID=9667;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Vardy T.L., Farid A.;
RT   "Nucleotide sequence variation of the mink preprolactin gene.";
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY249860; AAO92934.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
DR   InterPro; IPR001400; Somatotropin.
DR   Pfam; PF00103; hormone_1.
DR   PRINTS; PR00836; SOMATOTROPIN.
DR   PROSITE; PS00266; SOMATOTROPIN_1; 1.
DR   PROSITE; PS00338; SOMATOTROPIN_2; 1.
KW   Signal.
FT   SIGNAL        1     30       Potential.
FT   CHAIN        31     70       prolactin.
FT   CHAIN        71    106       prolactin.
FT   CHAIN       107    166       prolactin.
SQ   SEQUENCE   229 AA;  26194 MW;  D3ADDB618CCA29BC CRC64;

Query Match             84.1%;  Score 877;  DB 6;  Length 229;
Best Local Similarity   79.9%;  Pred. No. 1.5e-69;
Matches  159;  Conservative   25;  Mismatches   15;  Indels    0;  Gaps    0;

Qy         1 LPICPGGAARCQVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFITKAINSCHT 60
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Db        31 LPICPTGAVNCQVSLRDLFDRAVILSHYIHNLSSEMFNEFDKRYAQGRGFITKAINSCHT 90

Qy        61 SSLATPEDKEQAQQMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 120
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Db        91 SSLSTPEDKEQAQQIHHEDLLNLILRVLRSWNDPLYHLVSEVRGMQEAPDSILSRAIEIE 150

Qy       121 EQTKRLLEGMELIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSH 180
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Qy       181 KIDNYLKLLKCRIIHNNNC 199
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Db       211 KIDNYLKLLKCRIVYDSNC 229

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ID   Q8T110        PRELIMINARY;       PRT;   222 AA.
AC   Q8T110;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Prolactin precursor (Fragment).
GN   PRL.
OS   Taenia hydatigena.
OC   Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
OC   Cyclophyllidea; Taeniidae; Taenia.
OX   NCBI_TaxID=85431;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Chen Z.;
RT   "Cloning and analysis of the prolactin of cestode.";
RL   Chin. J. Vet. Sci. 22:157-159(2002).
DR   EMBL; AJ457817; CAD30063.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
DR   InterPro; IPR001400; Somatotropin.
DR   Pfam; PF00103; hormone_1.
DR   PRINTS; PR00836; SOMATOTROPIN.
DR   PROSITE; PS00266; SOMATOTROPIN_1; 1.
DR   PROSITE; PS00338; SOMATOTROPIN_2; 1.
KW   Signal.
FT   NON_TER       1      1
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OM protein - protein search, using sw model

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              GenCore version 5.1.6
         Copyright (c) 1993 - 2004  Compugen Ltd.
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Perfect score: 1043
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 389414 seqs, 51625971 residues

Total number of hits satisfying chosen parameters: 389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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6: /cgn2_6/ptodata/2/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Query Length	DB	ID	Description
1	1043	100.0	199	3	US-08-737-248-7	Sequence 7, Appli
2	1043	100.0	351	1	US-08-196-350-1	Sequence 1, Appli
3	887	85.0	199	3	US-08-737-248-10	Sequence 10, Appli
4	877	84.1	199	3	US-08-737-248-12	Sequence 12, Appli
5	876	84.0	199	3	US-08-737-248-8	Sequence 8, Appli
6	871	83.5	199	3	US-08-737-248-14	Sequence 14, Appli
7	797	76.4	199	3	US-08-737-248-13	Sequence 13, Appli
8	796	76.3	199	3	US-08-737-248-11	Sequence 11, Appli
9	786.5	75.4	198	3	US-08-737-248-6	Sequence 6, Appli
10	754	72.3	199	3	US-08-737-248-2	Sequence 2, Appli
11	754	72.3	199	3	US-08-737-248-4	Sequence 4, Appli
12	748	71.7	199	3	US-08-737-248-5	Sequence 5, Appli
13	737	70.7	199	3	US-08-737-248-9	Sequence 9, Appli
14	667	64.0	197	3	US-08-737-248-15	Sequence 15, Appli
15	667	64.0	197	3	US-08-737-248-17	Sequence 17, Appli
16	630	60.4	125	3	US-08-985-526-25	Sequence 25, Appli
17	630	60.4	253	3	US-08-985-526-27	Sequence 27, Appli
18	621	59.5	197	3	US-08-737-248-16	Sequence 16, Appli
19	370	35.5	199	3	US-08-737-248-23	Sequence 23, Appli
20	280	26.8	187	3	US-08-737-248-18	Sequence 18, Appli
21	280	26.8	187	3	US-08-737-248-19	Sequence 19, Appli
22	270	25.9	177	3	US-08-737-248-21	Sequence 21, Appli
23	269.5	25.8	188	3	US-08-737-248-20	Sequence 20, Appli
24	263	25.2	236	3	US-09-602-848-2	Sequence 2, Appli
25	245	23.5	223	3	US-09-602-848-4	Sequence 4, Appli
26	210.5	20.2	207	1	US-07-656-566-2	Sequence 2, Appli
27	210.5	20.2	231	1	US-07-656-566-3	Sequence 3, Appli
28	206	19.8	191	3	US-08-737-248-22	Sequence 22, Appl
29	192	18.4	191	1	US-08-093-383-3	Sequence 3, Appl
30	192	18.4	217	3	US-08-589-028-10	Sequence 10, Appl
31	192	18.4	217	3	US-08-784-582-10	Sequence 10, Appl
32	192	18.4	217	3	US-08-785-271-10	Sequence 11, Appl
33	192	18.4	217	4	US-08-759-628-11	Sequence 1, Appl
34	192	18.4	217	4	US-09-284-878-1	Sequence 1, Appl
35	192	18.4	191	4	US-09-511-024A-1	Sequence 29, Appl
36	190	18.2	191	1	US-07-885-689A-29	Sequence 2, Appl
37	190	18.2	191	1	US-09-539-746-2	Sequence 2, Appl
38	190	18.2	193	2	US-08-383-621-2	Sequence 2, Appl
39	190	18.2	193	3	US-08-459-906-2	Sequence 4, Appl
40	190	18.2	199	1	US-07-801-164A-4	Sequence 2, Appl
41	190	18.2	217	2	US-09-105-651-2	Sequence 9, Appl
42	189	18.1	191	4	US-09-511-024A-9	Sequence 51, Appl
43	189	18.1	217	2	US-08-469-486-51	Sequence 51, Appl
44	189	18.1	217	2	US-08-469-658-51	Sequence 2, Appl
45	185	17.7	191	4	US-09-511-024A-3	Sequence 3, Appl

ALIGNMENTS

RESULT 1
US-08-737-248-7
; Sequence 7, Application US/08737248
; Patent No. 6114305
; GENERAL INFORMATION:
; APPLICANT: Guemene, Daniel
; APPLICANT: Zadworny, David
; APPLICANT: Karatzas, Costas
; TITLE OF INVENTION: USE OF PROLACTIN FOR PREVENTING AND/OR
; TITLE OF INVENTION: TREATING BIRD BROODINESS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: WEISER & ASSOCIATES
;   STREET: 230 South Fifteenth Street, Suite 500
;   CITY: Philadelphia
;   STATE: PA
;   COUNTRY: USA
;   ZIP: 19102
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/737,248
;   FILING DATE: 28-APR-1997
;   CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/FR95/00576
;   FILING DATE: 03-MAY-1995
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: FR 94/05550
;   FILING DATE: 05-MAY-1994
; ATTORNEY/AGENT INFORMATION:
;   NAME: Weiser, Gerard J.
;   REGISTRATION NUMBER: 19,763
;   REFERENCE/DOCKET NUMBER: 989.6411P
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 215-875-8383
;   TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 7:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 199 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: linear
;   MOLECULE TYPE: protein
US-08-737-248-7

Query Match   100.0%; Score 1043; DB 3; Length 199;

Best Local Similarity 100.0%; Pred. No. 3.7e-98;
Matches 199; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Db   121  EQTKRLLEGMELIVSQVHPETKENEIYPVWSGLPSLQMADESRLSAYYNLLHCLRRDSH  180

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Db   181  KIDNYLKLLKCRIIHNNC 199
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RESULT 2
US-08-196-350-1
; Sequence 1, Application US/08196350
; Patent No. 5585099
; GENERAL INFORMATION:
; APPLICANT: Richards, Sue
; APPLICANT: Kaplan, Joanne
; APPLICANT: Moscicki, Richard
; TITLE OF INVENTION: PROLACTIN AS ADJUVANT
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Brad Salcedo
;   STREET: One Kendall Square
;   CITY: Cambridge
;   STATE: MA
;   COUNTRY: U.S.A.
;   ZIP: 02139
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/196,350
;   FILING DATE:
;   CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
;   NAME: Gosz, William G
;   REGISTRATION NUMBER: 27,787
;   REFERENCE/DOCKET NUMBER: GEN 4-1.0
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 6172527868
;   TELEFAX: 6173747225
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 351 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
; MOLECULE TYPE: peptide
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; ORIGINAL SOURCE:
;   ORGANISM: human prolactin
US-08-196-350-1

Query Match   100.0%; Score 1043; DB 1; Length 351;
Best Local Similarity 100.0%; Pred. No. 8.1e-98;
Matches 199; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Qy   121  EQTKRLLEGMELIVSQVHPETKENEIYPVWSGLPSLQMADESRLSAYYNLLHCLRRDSH 180
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Qy   181  KIDNYLKLLKCRIIHNNC 199
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Db   333  KIDNYLKLLKCRIIHNNC 351
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RESULT 3
US-08-737-248-10
; Sequence 10, Application US/08737248
; Patent No. 6114305
; GENERAL INFORMATION:
; APPLICANT: Guemene, Daniel
; APPLICANT: Zadworny, David
; APPLICANT: Karatzas, Costas
; TITLE OF INVENTION: USE OF PROLACTIN FOR PREVENTING AND/OR
; TITLE OF INVENTION: TREATING BIRD BROODINESS
; NUMBER OF SEQUENCES: 23
; CORRESPONDENCE ADDRESS:
;   ADDRESSEE: WEISER & ASSOCIATES
;   STREET: 230 South Fifteenth Street, Suite 500
;   CITY: Philadelphia
;   STATE: PA
;   COUNTRY: USA
;   ZIP: 19102
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/737,248
;   FILING DATE: 28-APR-1997
;   CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: PCT/FR95/00576
;   FILING DATE: 03-MAY-1995
; PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: FR 94/05550
;   FILING DATE: 05-MAY-1994
; ATTORNEY/AGENT INFORMATION:
;   NAME: Weiser, Gerard J.
;   REGISTRATION NUMBER: 19,763
;   REFERENCE/DOCKET NUMBER: 989.6411P
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 215-875-8383
;   TELEFAX: 215-875-8394
; INFORMATION FOR SEQ ID NO: 10:
; SEQUENCE CHARACTERISTICS:
;   LENGTH: 199 amino acids
;   TYPE: amino acid
;   STRANDEDNESS:
;   TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-737-248-10

Query Match   85.0%; Score 887; DB 3; Length 199;
Best Local Similarity   81.4%; Pred. No. 2.6e-82;
Matches 162; Conservative   22; Mismatches   15; Indels   0; Gaps   0;

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Qy    61  SSLATPEDKEQAQQMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 120
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Db    61
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                        GenCore version 5.1.6
                Copyright (c) 1993 - 2004 Compugen Ltd.

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Perfect score:  199
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Scoring table:  OLIGO
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Searched:       1586107 seqs, 282547505 residues

Word size :     0

Total number of hits satisfying chosen parameters:    1586107

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :  A_Geneseq_29Jan04:*
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            2: geneseqp1990s:*
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            7: geneseqp2003bs:*
            8: geneseqp2004s:*
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	199	100.0	199	2	AAY31764	Aay31764 Human pro
2	199	100.0	199	5	ABG94847	Abg94847 Human pro
3	199	100.0	200	2	AAW92258	Aaw92258 Human ant
4	199	100.0	227	2	AAR05231	Aar05231 AA sequen
5	199	100.0	227	4	AAG78336	Aag78336 Human pro
6	199	100.0	227	6	AAU28057	Aau28057 Novel hum
7	199	100.0	227	7	ADD48810	Add48810 Human Pro
8	199	100.0	351	2	AAR78691	Aar78691 Prolactin
9	185	93.0	359	2	AAR05805	Aar05805 DHFR-prol
10	178	89.4	228	2	AAW23626	Aaw23626 Prolactin
11	178	89.4	228	2	AAW23620	Aaw23620 Prolactin
12	136	68.3	173	6	AAO16662	Aao16662 Human ext
13	128	64.3	227	2	AAG78337	Aag78337 Mutant hu
14	124	62.3	125	2	AAW40299	Aaw40299 Human pro
15	124	62.3	227	1	AAP82079	Aap82079 Human pre
16	124	62.3	252	2	AAW40300	Aaw40300 Human con
17	111	55.8	199	6	ABU09878	Abu09878 Human pro
18	111	55.8	199	6	ABU09846	Abu09846 Human pro
19	103	51.8	199	2	AAW23629	Aaw23629 Human pro
20	101	50.8	199	3	AAY78428	Aay78428 Human pro
21	81	40.7	140	2	AAW92260	Aaw92260 Human ant
22	81	40.7	143	2	AAW92261	Aaw92261 Human ant
23	76	38.2	167	6	AAO16658	Aao16658 Human ext
24	68	34.2	125	2	AAY06194	Aay06194 Anti-angi
25	68	34.2	253	2	AAY06195	Aay06195 Anti-angi
26	65	32.7	124	2	AAW92259	Aaw92259 Human ant
27	36	18.1	258	4	AAU28245	Aau28245 Novel hum
28	31	15.6	199	6	ABU09864	Abu09864 Ancestral
29	28	14.1	56	5	AAE23373	Aae23373 Human pro
30	27	13.6	27	7	ADE82398	Ade82398 Human pro
31	26	13.1	199	6	ABU09854	Abu09854 Pig prola
32	26	13.1	199	6	ABU09855	Abu09855 Camel pro
33	26	13.1	199	6	ABU09858	Abu09858 Ancestral
34	25	12.6	199	6	ABU09851	Abu09851 Mink prol
35	25	12.6	199	6	ABU09856	Abu09856 Horse pro
36	24	12.1	24	7	ADE82402	Ade82402 Human pro
37	24	12.1	198	6	ABU09866	Abu09866 Bullfrog
38	24	12.1	198	6	ABU09861	Abu09861 Sea turtl
39	22	11.1	191	5	ABG94857	Abg94857 Human gro
40	21	10.6	21	7	ADE82400	Ade82400 Humari pro
41	20	10.1	20	2	AAW23639	Aaw23639 Human pro
42	19	9.5	199	2	AAR87090	Aar87090 Turkey pr
43	19	9.5	199	6	ABU09860	Abu09860 Turkey pr
44	19	9.5	426	2	AAR87091	Aar87091 Turkey pr
45	17	8.5	199	6	ABU09863	Abu09863 Alligator

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

ALIGNMENTS

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RESULT 1
AAY31764
ID   AAY31764 standard; protein; 199 AA.
XX
AC   AAY31764;
XX
DT   06-DEC-1999  (first entry)
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DE   Human prolactin.
XX
KW   Prolactin; human; variant; protein engineering.
XX
OS   Homo sapiens.
XX
FH   Key             Location/Qualifiers
FT   Misc-difference 59
FT                   /note= "optionally substituted by Phe in human prolactin
FT                   variant of Claim 8"
FT   Misc-difference 60
FT                   /note= "optionally substituted by Ser in human prolactin
FT                   variant of Claim 8"
FT   Misc-difference 61
FT                   /note= "optionally substituted by Glu in human prolactin
FT                   variant of Claim 8"
FT   Misc-difference 63
FT                   /note= "optionally substituted by Ile in human prolactin
FT                   variant of Claim 8"
FT   Misc-difference 64
FT                   /note= "optionally substituted by Pro in human prolactin
FT                   variant of Claim 8"
FT   Misc-difference 67
FT                   /note= "optionally substituted by Ser in human prolactin
FT                   variant of Claim 8"
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FT                   /note= "optionally substituted by Asn in human prolactin
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FT                   variant of Claim 8"
FT   Misc-difference 71
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FT                   /note= "optionally substituted by Lys in human prolactin
FT                   variant of Claim 8"
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Db   121  EQTKRLLEGMELIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSH  180

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AC   ABG94847;
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DT   03-DEC-2002  (first entry)
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DE   Human prolactin.
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KW   Growth hormone; placental lactogen; prolactin; active domain; hGH;
KW   structure-function relationship; segment-substituted polypeptide.
XX
OS   Homo sapiens.
XX
PN   US6428954-B1.
XX
PD   06-AUG-2002.
XX
PF   06-JUN-1995;  95US-00483039.
XX
PR   28-OCT-1988;  88US-00264611.
PR   26-OCT-1989;  89US-00428066.
PR   27-APR-1992;  92US-00875204.
PR   13-OCT-1992;  92US-00960227.
PR   02-FEB-1994;  94US-00190723.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Wells JA,  Cunningham BC;
XX
DR   WPI; 2002-696875/75.
XX
PT   Identifying active domains within cloned polypeptides of known amino acid
PT   sequence by substituting analog segments into the parent polypeptide is
PT   useful to determine the relationship between structure and function.
XX
PS   Disclosure; Fig 2; 86pp; English.
XX
CC   The invention relates to identifying an unknown active domain in a region
CC   of known amino acid sequence in a parent polypeptide e.g. human growth
CC   hormone (hGH) which has been cloned and has a pre-identified biological
CC   activity, where the active domain interacts with a target when the parent
CC   polypeptide is in its native-folded form and the interaction is
CC   responsible for the biological activity comprising: (a) comparing the
CC   amino acid sequence or polypeptide structure in the region of known amino
CC   acid sequence of hGH with the amino acid sequence or polypeptide
CC   structure in a region of known amino acid sequence of an analogue
CC   polypeptide (e.g. prolactin, placental lactogen or porcine growth
CC   hormone) which has at least 15% homology with hGH alpha-carbon
CC   coordinates within about 2-3.5 angstroms of hGH alpha-carbon coordinates
CC   for about 60% of the analogue sequence, where any interaction of the
CC   analogue with the target is different from target interaction with hGH;
CC   (b) substituting DNA encoding an analogous polypeptide segment from the
CC   analogue into DNA encoding the full length hGH, and expressing a segment-
CC   substituted polypeptide; (c) contacting the segment-substituted
CC   polypeptide with the target to determine interaction; (d) repeating steps
CC   (b) and (c) with a second analogous polypeptide segment; and (e)
CC   comparing the difference between activity of the first and second segment
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FT   Misc-difference  76
FT                    /note= "optionally substituted by Ser in human prolactin
FT                    variant of Claim 8"
FT   Misc-difference  77
FT                    /note= "optionally substituted by Asn in human prolactin
FT                    variant of Claim 8"
FT   Misc-difference  78
FT                    /note= "optionally substituted by Lys in human prolactin
FT                    variant of Claim 8"
FT   Misc-difference  79
FT                    /note= "optionally substituted by Glu in human prolactin
FT                    variant of Claim 8"
FT   Misc-difference  180
FT                    /note= "optionally substituted by Asp in human prolactin
FT                    variant of Claim 8"
FT   Misc-difference  184
FT                    /note= "optionally substituted by Thr in human prolactin
FT                    variant of Claim 8"
FT   Misc-difference  185
FT                    /note= "optionally substituted by Phe in human prolactin
FT                    variant of Claim 8"
FT   Misc-difference  187
FT                    /note= "optionally substituted by Arg in human prolactin
FT                    variant of Claim 8"
XX
PN   US5955346-A.
XX
PD   21-SEP-1999.
XX
PF   07-JUN-1995;  95US-00476999.
XX
PR   28-OCT-1988;  88US-00264611.
PR   26-OCT-1989;  89US-00428066.
PR   27-APR-1992;  92US-00875204.
PR   13-OCT-1992;  92US-00960227.
PR   02-FEB-1994;  94US-00190723.
XX
PA   (GETH ) GENENTECH INC.
XX
PI   Cunningham BC,  Wells JA;
XX
DR   WPI; 1999-560495/47.
XX
PT   Isolated nucleic acids encoding variants of human prolactin and placental
PT   lactogen useful for identifying active domains within those proteins.
XX
PS   Claim 7; Fig 2; 86pp; English.
XX
CC   This is the amino acid sequence of human prolactin. The invention
CC   provides a method for the systematic analysis of the structure and
CC   function of polypeptides by identifying active domains which influence
CC   the activity of the polypeptide with a target substance, and a method for
CC   identifying the active amino acid residues within the active domain of a
CC   polypeptide. It also provides polypeptide variants comprising segment-
CC   substituted and residue-substituted growth hormones, prolactins and
CC   placental lactogens. Claimed variants of human prolactin have 1-19 amino
CC   acid substitutions when compared to the wild-type sequence, selected from
CC   H59F, T60S, S61E, L61I, A64P, E67S, D68N, K69R, Q71E, A72T, M75K, N76S,
CC   Q77N, K78L, D79E, H180D, N184T, Y185F and K185R. These mutations
CC   inactivate the active domains and binding sites of the protein.
CC   Identifying receptor binding sites in hormones permits the rational
CC   design of receptor specific variants. Nucleic acids encoding the
CC   variants, expression vectors and host cells are also claimed
XX
SQ   Sequence 199 AA;

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Matches   199;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps   0;

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OM protein - protein search, using sw model

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            GenCore version 5.1.6
       Copyright (c) 1993 - 2004 Compugen Ltd.

Run on:   September 13, 2004, 12:25:35 ; Search time 40 Seconds
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                         478.553 Million cell updates/sec

Title:        US-10-735-594-1
Perfect score: 199
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Scoring table:  OLIGO
                Gapop 60.0 , Gapext 60.0

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Word size :   0

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Minimum DB seq length: 0
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Post-processing: Listing first 45 summaries

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          4:  pir4:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	199	100.0	227	1	LCHU	prolactin precurso
2	195	98.0	228	2	A61042	prolactin precurso
3	26	13.1	199	2	S15131	prolactin - Arabia
4	26	13.1	229	1	LCPG	prolactin precurso
5	25	12.6	175	2	S18882	prolactin - Americ
6	25	12.6	199	1	LCHO	prolactin - horse
7	24	12.1	134	1	I51233	prolactin - Japane
8	24	12.1	198	1	A60620	prolactin - green
9	24	12.1	207	2	A60969	prolactin precurso
10	19	9.5	229	2	A61133	prolactin precurso
11	19	9.5	229	2	A60972	prolactin precurso
12	17	8.5	229	2	JC4631	prolactin precurso
13	16	8.0	199	2	PN0128	prolactin - sel wh
14	14	7.0	226	1	LCRT	prolactin precurso
15	13	6.5	228	1	LCMS	prolactin precurso
16	12	6.0	229	1	LCBO	prolactin precurso
17	12	6.0	229	1	LCSH	prolactin precurso
18	12	6.0	229	2	I83982	prolactin - goat
19	10	5.0	188	2	B28106	prolactin, 24K - M
20	10	5.0	199	2	JS0430	prolactin - elepha
21	10	5.0	212	2	A32477	prolactin I precur
22	10	5.0	212	2	I51034	prolactin-I - Moza
23	9	4.5	200	2	S34604	prolactin - marble
24	9	4.5	209	2	S30541	prolactin precurso
25	8	4.0	177	2	A28106	prolactin, 20K - M
26	8	4.0	187	2	S06677	prolactin II - chu
27	8	4.0	187	2	S02304	prolactin I - chum
28	8	4.0	200	2	B32477	prolactin II precu
29	8	4.0	207	2	S21965	prolactin - silver
30	8	4.0	210	1	S01435	prolactin precurso
31	8	4.0	210	2	I51084	prolactin precurso
32	8	4.0	210	2	PN0092	prolactin precurso
33	8	4.0	210	2	S16765	prolactin precurso
34	8	4.0	210	2	A31364	prolactin precurso
35	8	4.0	210	2	S34351	prolactin - Atlant
36	8	4.0	210	2	S52475	prolactin - Atlant
37	8	4.0	210	2	S71486	prolactin precurso
38	8	4.0	211	2	S00359	prolactin precurso
??			212	2	I51275	prolactin precurso
40	8	4.0	226	2	A49159	prolactin - golden
41	8	4.0	227	2	A24911	prolactin-like pro
42	8	4.0	324	2	T32535	hypothetical prote
43	8	4.0	547	2	AE1830	hypothetical prote
44	8	4.0	751	2	AI3392	phosphoribosylform
45	8	4.0	3938	2	T42761	Bassoon protein -

ALIGNMENTS

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prolactin precursor [validated] - human
C;Species: Homo sapiens (man)
C;Date: 30-Jun-1979 #sequence_revision 23-Oct-1981 #text_change 08-Dec-2000
C;Accession: A90998; A92318; A28867; PN0089; A92762; A92177; A01505
R;Truong, A.T.; Duez, C.; Belayew, A.; Renard, A.; Pictet, R.; Bell, G.I.; Martial, J.A.
EMBO J. 3, 429-437, 1984
A;Title: Isolation and characterization of the human prolactin gene.
A;Reference number: A90998; MUID:8182507; PMID:6325171
A;Accession: A90998
A;Molecule type: DNA
A;Residues: 1-227 <TRU>
R;Cooke, N.E.; Coit, D.; Shine, J.; Baxter, J.D.; Martial, J.A.
J. Biol. Chem. 256, 4007-4016, 1981
A;Title: Human prolactin: cDNA structural analysis and evolutionary comparisons.
A;Reference number: A92318; MUID:81168179; PMID:6260780
A;Accession: A92318
A;Molecule type: mRNA
A;Residues: 1-227 <COO>
A;Cross-references: GB:V00566; GB:J00299; NID:g34210; GB:J00566; NID:g34210; PIDN:CAA23829.1; PID:g34211
R;Takahashi, H.; Nabeshima, Y.; Ogata, K.; Takeuchi, S.
J. Biochem. 95, 1491-1499, 1984
A;Title: Molecular cloning and nucleotide sequence of DNA complementary to human decidua
A;Reference number: A28867; MUID:84264464; PMID:6146607
A;Accession: A28867
A;Molecule type: mRNA
A;Residues: 1-205,'H',207-227 <TAK>
A;Cross-references: EMBL:M29386
A;Note: the authors translated the codon CAT for residue 206 as Asp
R;Mertvetsov, N.P.; Golovin, S.Y.; Zelenin, S.M.; Morozova, T.V.; Karginov, V.A.; Chekhr
Bioorg. Khim. 13, 1687-1690, 1987
A;Title: Synthesis, cloning and sequencing of cDNA complementary to mRNA of prolactin fr
A;Reference number: PN0089; MUID:88221681; PMID:3450284
A;Accession: PN0089
A;Molecule type: mRNA
A;Residues: 45-227 <MER>
A;Experimental source: pituitary gland
R;Shome, B.; Parlow, A.F.
J. Clin. Endocrinol. Metab. 45, 1112-1115, 1977
A;Title: Human pituitary prolactin (hPRL): the entire linear amino acid sequence.
A;Reference number: A92762; MUID:78046207; PMID:925136
A;Accession: A92762
A;Molecule type: protein
A;Residues: 29-109,'VS',112,'L',115-132,'X',134-171,'D',173-189,'SE',192-227 <SHO>
R;Jacobs, J.W.; Niall, H.D.
J. Biol. Chem. 250, 3629-3636, 1975
A;Title: High sensitivity automated sequence determination of polypeptides.
A;Reference number: A92177; MUID:75151509; PMID:126929
A;Accession: A92177
A;Molecule type: protein
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A;Residues: 29-52,'L' <JAC>
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A;Gene: GDB:PRL
A;Cross-references: GDB:119517; OMIM:176760
A;Map position: 6p22.2-6p22.1
A;Introns: 9/3; 68/3; 104/3; 164/3
C;Superfamily: prolactin
C;Keywords: anterior pituitary; hormone; lactation; placenta
F;1-28/Domain: signal sequence #status predicted <SIG>
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F;32-39,86-202,219-227/Disulfide bonds: #status predicted

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Db   89 SSLATPEDKEQAQQMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 148

Qy  121 EQTKRLLEGMELIVSQVHPETKENEIYPVWSGLPSLQMADESRLSAYYNLLHCLRRDSH 180
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Db  149 EQTKRLLEGMELIVSQVHPETKENEIYPVWSGLPSLQMADESRLSAYYNLLHCLRRDSH 208

Qy  181 KIDNYLKLLKCRIIHNNNC 199
          |||||||||||||||||||
Db  209 KIDNYLKLLKCRIIHNNNC 227
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RESULT 2
A61402
prolactin precursor, placental (clone 204) - human
C;Species: Homo sapiens (man)
C;Date: 09-Sep-1994 #sequence_revision 09-Sep-1994 #text_change 16-Feb-1997
C;Accession: A61402
R;Hiraoka, Y.; Tatsumi, K.; Shiozawa, M.; Aiso, S.; Fukasawa, T.; Yasuda, K.; Miyai, K.
Mol. Cell. Endocrinol. 75, 71-80, 1991
A;Title: A placenta-specific 5' non-coding exon of human prolactin.
A;Reference number: A61402; MUID:91267286; PMID:2050267
A;Accession: A61402
A;Status: preliminary: not compared with conceptual translation
A;Molecule type: mRNA
A;Residues: 1-228 <HIR>
C;Superfamily: prolactin
C;Keywords: alternative splicing
F;87-203,220-228/Disulfide bonds: #status predicted

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Db   34 PGGAARCQVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFITKAINSCHTSSLA 93

Qy   65 TPEDKEQAQQMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIEEQTK 124
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Db  154 RLLEGMELIVSQVHPETKENEIYPVWSGLPSLQMADESRLSAYYNLLHCLRRDSHKIDN 213

Qy  185 YLKLLKCRIIHNNNC 199
          |||||||||||||||
Db  214 YLKLLKCRIIHNNNC 228
```

RESULT 3

S15131
prolactin - Arabian camel
C;Species: Camelus dromedarius (Arabian camel)
C;Date: 19-Mar-1997 #sequence_revision 19-Mar-1997 #text_change 11-May-2000
C;Accession: S15131; A60513
R;Martinat, N.; Huet, J.C.; Nespoulous, C.; Combarnous, Y.; Pernollet, J.C.
Biochim. Biophys. Acta 1077, 339-345, 1991
A;Title: Determination of the primary and secondary structures of the dromedary (Camelus
A;Reference number: S15131; MUID:91230144; PMID:2029533
A;Accession: S15131
A;Status: preliminary
A;Molecule type: protein
A;Residues: 1-199 <MAR>
R;Martinat, N.; Anouassi, A.; Huet, J.C.; Pernollet, J.C.; Combarnous, Y.
Comp. Biochem. Physiol. B 97, 667-674, 1990
A;Title: Purification and characterization of glycosylated and non-glycosylated forms of
A;Reference number: A60513; MUID:91199560; PMID:2085952
A;Accession: A60513
A;Molecule type: protein
A;Residues: 1-40 <MA2>
C;Superfamily: prolactin
C;Keywords: anterior pituitary; hormone; lactation; placenta

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Query Match             13.1%;  Score 26;  DB 2;  Length 199;
Best Local Similarity  100.0%;  Pred. No. 2.4e-19;
Matches 26;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy  169 YNLLHCLRRDSHKIDNYLKLLKCRII 194
          ||||||||||||||||||||||||||
Db  169 YNLLHCLRRDSHKIDNYLKLLKCRII 194
```

RESULT 4
LCPG
prolactin precursor - pig
C;Species: Sus scrofa domestica (domestic pig)
C;Date: 24-Apr-1984 #sequence_revision 27-Jun-1994 #text_change 18-Jun-1999
C;Accession: S04077; A60971; A01507
R;Schulz-Aellen, M.F.; Schmid, E.; Movva, R.N.
Nucleic Acids Res. 17, 3295, 1989
A;Title: Nucleotide sequence of porcine preprolactin cDNA.
A;Reference number: S04077; MUID:89263739; PMID:2726463
A;Accession: S04077
A;Molecule type: mRNA
A;Residues: 1-229 <SCH>
A;Cross-references: EMBL:X14068; NID:g2082; PIDN:CAA32231.1; PID:g2083
R;Kato, Y.; Hirai, T.; Kato, T.
J. Mol. Endocrinol. 4, 135-142, 1990
A;Title: Molecular cloning of cDNA for porcine prolactin precursor.
A;Reference number: A60971; MUID:90262633; PMID:2344390
A;Accession: A60971
A;Molecule type: mRNA
A;Residues: 1-3,'R',5,'X',7-42,'V',44-229 <KAT>
R;Li, C.H.
Int. J. Pept. Protein Res. 8, 205-224, 1976
A;Title: Studies on pituitary lactogenic hormone. The primary structure of the porcine h
A;Reference number: A91770; MUID:76189476; PMID:1270193
A;Accession: A01507
A;Molecule type: protein
A;Residues: 31-42,'V',44-151,'E',153-225,'N',227-229 <LIC>
C;Superfamily: prolactin
C;Keywords: anterior pituitary; hormone; lactation; placenta
F;1-30/Domain: signal sequence #status predicted <SIG>
F;31-229/Product: prolactin #status experimental <MAT>
F;34-41,88-204,221-229/Disulfide bonds: #status experimental

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Query Match             13.1%;  Score 26;  DB 1;  Length 229;
Best Local Similarity  100.0%;  Pred. No. 2.7e-19;
Matches 26;  Conservative  0;  Mismatches  0;  Indels  0;  Gaps  0;

Qy  169 YNLLHCLRRDSHKIDNYLKLLKCRII 194
          ||||||||||||||||||||||||||
Db  199 YNLLHCLRRDSHKIDNYLKLLKCRII 224
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```
            GenCore version 5.1.6
        Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:  September 13, 2004, 12:17:24 ; Search time 24 Seconds
                                        (without alignments)
                        431.748 Million cell updates/sec

Title:         US-10-735-594-1
Perfect score: 199
Sequence:      1 LPICPGGAARCQVTLRDLFD.........HKIDNVLKLLKCRIIHHNNC 199

Scoring table: OLIGO
               Gapop 60.0 , Gapext 60.0

Searched:      141681 seqs, 52070155 residues

Word size :    0

Total number of hits satisfying chosen parameters:        141681

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :     SwissProt_42:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.
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SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	199	100.0	227	1	PRL_HUMAN	P01236 homo sapien
2	52	26.1	227	1	PRL_MACMU	P55151 macaca mula
3	26	13.1	199	1	PRL_CAMDR	P22393 camelus dro
4	26	13.1	227	1	PRL_RABIT	Q28632 oryctolagus
5	26	13.1	229	1	PRL_PIG	P01238 sus scrofa
6	25	12.6	193	1	PRL_MUSVI	P29234 mustela vis
7	25	12.6	199	1	PRL_HORSE	P12420 equus cabal
8	24	12.1	134	1	PRL_BUFJA	P43001 bufo japoni
9	24	12.1	198	1	PRL_CHEMY	P33090 chelonia my
10	24	12.1	228	1	PRL_MONDO	O62819 monodelphis
11	24	12.1	228	1	PRL_TRIVU	O62781 trichosurus
12	19	9.5	229	1	PRL_CHICK	P14676 gallus gall
13	19	9.5	229	1	PRL_MELGA	P17572 meleagris g
14	17	8.5	199	1	PRL1_ALLMI	P55751 alligator m
15	17	8.5	199	1	PRL1_CRONO	P55753 crocodylus
16	17	8.5	199	1	PRL2_ALLMI	P55752 alligator m
17	17	8.5	199	1	PRL2_CRONO	P55754 crocodylus
18	17	8.5	229	1	PRL_FELCA	P46403 felis silve
19	16	8.0	199	1	PRL_BALBO	P33089 balaenopter
20	14	7.0	226	1	PRL_RAT	P01237 rattus norv
21	13	6.5	226	1	PRL_MOUSE	P06879 mus musculu
22	12	6.0	229	1	PRL_BOVIN	P01239 bos taurus
23	12	6.0	229	1	PRL_CAPHI	Q28818 capra hircu
24	12	6.0	229	1	PRL_SHEEP	P01240 ovis aries
25	10	5.0	199	1	PRL_LOXAF	P10765 loxodonta a
26	10	5.0	212	1	PRL1_OREMO	P09319 oreochromis
27	9	4.5	200	1	PRL_PROAT	P33091 protopterus
28	9	4.5	209	1	PRL_ANGAN	P33096 anguilla an
29	8	4.0	200	1	PRL2_OREMO	P09318 oreochromis
30	8	4.0	207	1	PRL_HYPMO	P35395 hypophthalm
31	8	4.0	210	1	PRL2_ONCKE	P09584 oncorhynchu
32	8	4.0	210	1	PRL2_ONCTS	Q91364 oncorhynchu
33	8	4.0	210	1	PRL_CARAU	P87495 carassius a
34	8	4.0	210	1	PRL_CORAU	P34181 coregonus a
35	8	4.0	210	1	PRL_CYPCA	P09585 cyprinus ca
36	8	4.0	210	1	PRL_HYPNO	P29235 hypophthalm
37	8	4.0	210	1	PRL_ONCMY	P21993 oncorhynchu
38	8	4.0	210	1	PRL_SALSA	P48096 salmo salar
39	8	4.0	211	1	PRL1_ONCKE	P09583 oncorhynchu
40	8	4.0	211	1	PRL_PAROL	Q9ygv6 paralichthy
41	8	4.0	212	1	PRL_DICLA	P48249 dicentrarch
42	8	4.0	212	1	PRL_ICTPU	P51904 ictalurus p
43	8	4.0	212	1	PRL_SPAAU	O93337 sparus aura
44	8	4.0	226	1	PRL_MESAU	P37884 mesocricetu
45	8	4.0	227	1	PRRA_RAT	P09320 rattus norv

ALIGNMENTS

```
RESULT 1
PRL_HUMAN
ID   PRL_HUMAN      STANDARD;      PRT;   227 AA.
AC   P01236; Q15199; Q92996;
DT   21-JUL-1986 (Rel. 01, Created)
DT   21-JUL-1986 (Rel. 01, Last sequence update)
DT   15-MAR-2004 (Rel. 43, Last annotation update)
DE   Prolactin precursor (PRL).
GN   PRL.
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=8182507; PubMed=6325171;
RA   Truong A.T., Duez C., Belayew A., Renard A., Pictet R.L., Bell G.I.,
RA   Martial J.A.;
RT   "Isolation and characterization of the human prolactin gene.";
RL   EMBO J. 3:429-437(1984).
RN   [2]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=8168179; PubMed=6260780;
RA   Cooke N.E., Coit D., Shine J., Baxter J.D., Martial J.A.;
RT   "Human prolactin. cDNA structural analysis and evolutionary
RT   comparisons.";
RL   J. Biol. Chem. 256:4007-4016(1981).
RN   [3]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=9267286; PubMed=2050267;
RA   Hiraoka Y., Tatsumi K., Shiozawa M., Aiso S., Fukasawa T., Yasuda K.,
RA   Miyai K.;
RT   "A placenta-specific 5'non-coding exon of human prolactin.";
RL   Mol. Cell. Endocrinol. 75:71-80(1990).
RN   [4]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Testis;
RX   MEDLINE=22388257; PubMed=12477932;
RA   Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA   Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA   Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA   Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA   Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA   Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA   Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA   Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA   Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA   Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA   Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA   Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A.,
RA   Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA   Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA   Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA   Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E.,
RA   Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT   "Generation and initial analysis of more than 15,000 full-length human
```

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RT   and mouse cDNA sequences.";
RL   Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN   [5]
RP   SEQUENCE OF 11-227 FROM N.A.
RX   MEDLINE=84264464; PubMed=6146607;
RA   Takahashi H., Nabeshima Y., Ogata K., Takeuchi S.;
RT   "Molecular cloning and nucleotide sequence of DNA complementary to
RT   human decidual prolactin mRNA.";
RL   J. Biochem. 95:1491-1499(1984).
RN   [6]
RP   SEQUENCE OF 11-201 FROM N.A.
RC   TISSUE=Breast;
RX   MEDLINE=97411082; PubMed=9266104;
RA   Shaw-Bruha C.M., Pirrucello S.J., Shull J.D.;
RT   "Expression of the prolactin gene in normal and neoplastic human
RT   breast tissues and human mammary cell lines: promoter usage and
RT   alternative mRNA splicing.";
RL   Breast Cancer Res. Treat. 44:243-253(1997).
RN   [7]
RP   SEQUENCE OF 29-227.
RX   MEDLINE=78046207; PubMed=925136;
RA   Shome B., Parlow A.F.;
RT   "Human pituitary prolactin (hPRL): the entire linear amino acid
RT   sequence.";
RL   J. Clin. Endocrinol. Metab. 45:1112-1115(1977).
RN   [8]
RP   SEQUENCE OF 29-53.
RX   MEDLINE=75151509; PubMed=1126929;
RA   Jacobs J.W., Niall H.D.;
RT   "High sensitivity automated sequence determination of polypeptides.";
RL   J. Biol. Chem. 250:3629-3636(1975).
CC   -!- FUNCTION: Prolactin acts primarily on the mammary gland by
CC       promoting lactation.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the somatotropin/prolactin family.
CC   -!- CAUTION: Ref.3 sequence differs from that shown due to a
CC       frameshift in position 8.
CC   --------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
CC   modified and this statement is not removed. Usage by and for commercial
CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------
DR   EMBL; X00540; CAA25214.1; -.
DR   EMBL; X00541; CAA25214.1; JOINED.
DR   EMBL; X00543; CAA25214.1; JOINED.
DR   EMBL; X00544; CAA25214.1; JOINED.
DR   EMBL; V00566; CAA23829.1; -.
DR   EMBL; X54393; CAA38263.1; ALT_FRAME.
DR   EMBL; X54393; CAA38264.1; ALT_FRAME.
DR   EMBL; BC015850; AAH15850.1; -.
DR   EMBL; M29386; AAA60173.1; -.
DR   EMBL; D00411; BAA00312.1; -.
DR   EMBL; U75583; AAB70858.1; -.
DR   PIR; A90998; LCHU.
DR   HSSP; Q28632; 1AN3.
DR   Genew; HGNC:9445; PRL.
DR   MIM; 176760; -.
DR   GO; GO:0005148; F:prolactin receptor binding; TAS.
DR   GO; GO:0008283; P:cell proliferation; TAS.
DR   GO; GO:0007166; P:cell surface receptor linked signal transdu. .; TAS.
DR   GO; GO:0007516; P:hemocyte development; TAS.
DR   InterPro; IPR001400; Somatotropin.
DR   Pfam; PF00103; hormone; 1.
DR   PRINTS; PR00836; SOMATOTROPIN.
DR   PROSITE; PS00266; SOMATOTROPIN_1; 1.
DR   PROSITE; PS00338; SOMATOTROPIN_2; 1.
KW   Hormone; Lactation; Pituitary; Signal; Glycoprotein.
FT   SIGNAL        1     28
FT   CHAIN        29    227       PROLACTIN.
```

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FT   DISULFID     32     39                    BY SIMILARITY.
FT   DISULFID     86    202                    BY SIMILARITY.
FT   DISULFID    219    227                    BY SIMILARITY.
FT   CARBOHYD     59     59                    N-LINKED (GLCNAC...).
FT   CONFLICT     42     42       T -> A (IN REF. 6).
FT   CONFLICT    110    111       SL -> VS (IN REF. 7).
FT   CONFLICT    113    114       VS -> L (IN REF. 7).
FT   CONFLICT    118    118       S -> P (IN REF. 6).
FT   CONFLICT    148    148       E -> Q (IN REF. 5).
FT   CONFLICT    172    172       N -> D (IN REF. 7).
FT   CONFLICT    190    191       ES -> SE (IN REF. 7).
FT   CONFLICT    206    206       D -> H (IN REF. 5).
SQ   SEQUENCE   227 AA;  25876 MW;  952BA1B6A955527 CRC64;
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Query Match             100.0%;  Score 199;  DB 1; Length 227;
Best Local Similarity   100.0%;  Pred. No. 2.3e-203;
Matches  199;  Conservative    0;  Mismatches    0;  Indels    0;  Gaps    0;

Qy      1  LPICPGGAARCQVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFITKAINSCHT  60
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Db     29  LPICPGGAARCQVTLRDLFDRAVVLSHYIHNLSSEMFSEFDKRYTHGRGFITKAINSCHT  88

Qy     61  SSLATPEDKEQAQQMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE  120
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db     89  SSLATPEDKEQAQQMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE  148

Qy    121  EQTKRLLEGMELIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSH  180
           ||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db    149  EQTKRLLEGMELIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSH  208

Qy    181  KIDNYLKLLKCRIIHNNNC  199
           |||||||||||||||||||
Db    209  KIDNYLKLLKCRIIHNNNC  227
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```
RESULT 2
PRL_MACMU
ID   PRL_MACMU     STANDARD;      PRT;    227 AA.
AC   P55151;
DT   01-OCT-1996 (Rel. 34, Created)
DT   01-OCT-1996 (Rel. 34, Last sequence update)
DT   28-FEB-2003 (Rel. 41, Last annotation update)
DE   Prolactin precursor (PRL).
GN   PRL.
OS   Macaca mulatta (Rhesus macaque).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae; Macaca.
OX   NCBI_TaxID=9544;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Decidua;
RX   MEDLINE=94220570; PubMed=8167226;
RA   Brown N.A., Bethea C.L.;
RT   "Cloning of decidual prolactin from rhesus macaque.";
RL   Biol. Reprod. 50:543-552(1994).
CC   -!- FUNCTION: Prolactin acts primarily on the mammary gland by
CC       promoting lactation.
CC   -!- SUBCELLULAR LOCATION: Secreted.
CC   -!- SIMILARITY: Belongs to the somatotropin/prolactin family.
CC   --------------------------------------------------------------------
CC   This SWISS-PROT entry is copyright. It is produced through a collaboration
CC   between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC   the European Bioinformatics Institute. There are no restrictions on its
CC   use by non-profit institutions as long as its content is in no way
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CC   entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC   or send an email to license@isb-sib.ch).
CC   --------------------------------------------------------------------
DR   EMBL; U09018; AAA18471.1; -.
DR   HSSP; Q28632; 1AN3.
DR   InterPro; IPR001400; Somatotropin.
DR   Pfam; PF00103; hormone; 1.
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                    GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on:      September 13, 2004, 12:24:30 ; Search time 117 Seconds
                                (without alignments)
                                536.651 Million cell updates/sec

Title:           US-10-735-594-1
Perfect score:   199
Sequence:        1 LPICPGGAARCCVTLRDLFD.........HKIDNYLKLLKCRIIHNNNC 199

Scoring table:   OLIGO
                 Gapop 60.0 , Gapext 60.0

Searched:        1017041 seqs, 31551B202 residues

Word size :      0

Total number of hits satisfying chosen parameters:        1017041

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

Database :       SPTREMBL_25:*
                 1: sp_archea:*
                 2: sp_bacteria:*
                 3: sp_fungi:*
                 4: sp_human:*
                 5: sp_invertebrate:*
                 6: sp_mammal:*
                 7: sp_mhc:*
                 8: sp_organelle:*
                 9: sp_phage:*
                10: sp_plant:*
                11: sp_rodent:*
                12: sp_virus:*
                13: sp_vertebrate:*
                14: sp_unclassified:*
                15: sp_rvirus:*
                16: sp_bacteriap:*
                17: sp_archeap:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                          SUMMARIES
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Result No.	Score	% Query Match	Length	DB	ID	Description
1	44	22.1	199	6	Q9TS41	Q9ts41 papio (babo
2	35	17.6	44	4	Q9UDA3	Q9uda3 homo sapien
3	29	14.6	222	8	Q8T110	Q8t110 taenia hyda
4	25	12.6	229	6	Q8HXS1	Q8hxs1 ailuropoda
5	25	12.6	229	6	Q864R8	Q864r8 mustela vis
6	24	12.1	214	13	Q8JFX6	Q8jfx6 rana catesb
7	23	11.6	233	13	Q7T1A5	Q7t1a5 ambystoma b
8	16	8.0	16	4	Q9UP51	Q9up51 homo sapien
9	14	7.0	161	11	Q63293	Q63293 rattus norv
10	13	6.5	225	11	Q9CPQ0	Q9cpq0 mus musculu
11	13	6.5	225	11	Q9CYL2	Q9cyl2 mus musculu
12	13	6.5	226	11	Q9CYL8	Q9cyl8 mus musculu
13	13	6.5	228	11	Q9CPQ2	Q9cpq2 mus musculu
14	12	6.0	103	13	Q9PSP9	Q9psp9 xenopus lae
15	12	6.0	103	13	Q9PSP8	Q9psp8 xenopus lae
16	12	6.0	229	13	Q902B1	Q902b1 gallus gall

No.				ID		Description
17	11	5.5	225	11	Q9QZL1	Q9qzl1 microtus mo
18	10	5.0	61	13	Q9PWF9	Q9pwf9 coturnix co
19	9	4.5	209	13	Q7ZZV3	Q7zzv3 anguilla ja
20	9	4.5	220	11	Q9RO8	Q9ro8 rattus norv
21	9	4.5	227	11	Q8K3W4	Q8k3w4 rattus norv
22	8	4.0	20	13	Q9PWQ4	Q9pwq4 gallus gall
23	8	4.0	166	13	Q805E3	Q805e3 periophthal
24	8	4.0	210	13	Q91170	Q91170 oncorhynchu
25	8	4.0	210	13	Q801K3	Q801k3 brachydanio
26	8	4.0	211	13	Q7T1A8	Q7t1a8 perca flave
27	8	4.0	212	13	Q902N5	Q902n5 heteropneus
28	8	4.0	212	13	Q7ZZM0	Q7zzm0 sparus aura
29	8	4.0	227	11	Q35256	Q35256 mus musculu
30	8	4.0	251	11	Q8CJ42	Q8cj42 rattus norv
31	8	4.0	324	5	O44166	O44166 caenorhabdi
32	8	4.0	362	2	Q56591	Q56591 vibrio angu
33	8	4.0	547	16	Q8Z0A9	Q8z0a9 anabaena sp
34	8	4.0	740	16	Q8G183	Q8g183 brucella su
35	8	4.0	1139	16	Q89YK7	Q89yk7 bacteroides
36	8	4.0	1510	10	Q7XWS5	Q7xws5 oryza sativ
37	8	4.0	3851	4	O43161	O43161 homo sapien
38	8	4.0	3926	4	Q9UPA5	Q9upa5 homo sapien
39	8	4.0	3938	11	O88778	O88778 rattus norv
40	8	4.0	3942	11	O88737	O88737 mus musculu
41	7	3.5	18	11	Q9JJM8	Q9jjm8 rattus norv
42	7	3.5	32	6	Q9TRI8	Q9tri8 macropus ru
43	7	3.5	57	5	Q9VE38	Q9ve38 drosophila
44	7	3.5	58	16	Q87TI7	Q87ti7 vibrio para
45	7	3.5	66	13	Q9I889	Q9i889 oncorhynchu

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                                          ALIGNMENTS

RESULT 1
Q9TS41
ID   Q9TS41        PRELIMINARY;        PRT;     199 AA.
AC   Q9TS41;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Prolactin.
OS   Papio (baboons).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
OC   Cercopithecinae.
OX   NCBI_TaxID=9554;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=92037387; PubMed=1935793;
RA   Cole E.S., Nichols E.H., Lauziere K., Edmunds T., McPherson J.M.;
RT   "Characterization of the microheterogeneity of recombinant primate
RT   prolactin: implications for posttranslational modifications of the
RT   hormone in vivo.";
RL   Endocrinology 129:2639-2646(1991).
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
DR   InterPro; IPR001400; Somatotropin.
DR   Pfam; PF00103; hormone; 1.
DR   PRINTS; PR00836; SOMATOTROPIN.
DR   PROSITE; PS00266; SOMATOTROPIN_1; 1.
DR   PROSITE; PS00338; SOMATOTROPIN_2; 1.
SQ   SEQUENCE 199 AA;  22850 MW;  872A8935FEA43B67 CRC64;

Query Match             22.1%;  Score 44;  DB 6;  Length 199;
Best Local Similarity  100.0%;  Pred. No. 3.9e-37;
  Matches   44;   Conservative    0;   Mismatches    0;   Indels    0;   Gaps    0;

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RESULT 2
Q9UDA3
ID   Q9UDA3   PRELIMINARY;   PRT;   44 AA.
AC   Q9UDA3;
DT   01-MAY-2000 (TrEMBLrel. 13, Created)
DT   01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Prolactin (Fragment).
OS   Homo sapiens (Human).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX   NCBI_TaxID=9606;
RN   [1]
RP   SEQUENCE FROM N.A.
RX   MEDLINE=93292510; PubMed=8513798;
RA   Goffin V., Struman I., Goormaghtigh E., Martial J.A.;
RT   "The addition of nine residues at the C-terminus of human prolactin
RT   drastically alters its biological properties.";
RL   Eur. J. Biochem. 214:483-490(1993).
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
DR   InterPro; IPR001400; Somatotropin.
DR   Pfam; PF00103; hormone_1.
DR   PROSITE; PS00338; SOMATOTROPIN_2; 1.
SQ   SEQUENCE   44 AA; 5416 MW; 707E91C66398F4BF CRC64;

Query Match   17.6%; Score 35; DB 4; Length 44;
Best Local Similarity   100.0%; Pred. No. 2.4e-28;
Matches   35; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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RESULT 3
Q8T110
ID   Q8T110   PRELIMINARY;   PRT;   222 AA.
AC   Q8T110;
DT   01-JUN-2002 (TrEMBLrel. 21, Created)
DT   01-JUN-2002 (TrEMBLrel. 21, Last sequence update)
DT   01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
DE   Prolactin precursor (Fragment).
GN   PRL.
OS   Taenia hydatigena.
OC   Eukaryota; Metazoa; Platyhelminthes; Cestoda; Eucestoda;
OC   Cyclophyllidea; Taeniidae; Taenia.
OX   NCBI_TaxID=85431;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Chen Z.;
RT   "Cloning and analysis of the prolactin of cestode.";
RL   Chin. J. Vet. Sci. 22:157-159(2002).
DR   EMBL; AJ457817; CAD30063.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
DR   InterPro; IPR001400; Somatotropin.
DR   Pfam; PF00103; hormone_1.
DR   PRINTS; PR00836; SOMATOTROPIN.
DR   PROSITE; PS00266; SOMATOTROPIN_1; 1.
DR   PROSITE; PS00338; SOMATOTROPIN_2; 1.
KW   Signal.
FT   NON_TER   1   1
FT   SIGNAL   <1   22   POTENTIAL.
FT   CHAIN   23   222   PROLACTIN.
SQ   SEQUENCE 222 AA; 25346 MW; 310BFAFI8799F332 CRC64;

Query Match   14.6%; Score 29; DB 5; Length 222;
Best Local Similarity   100.0%; Pred. No.1.6e-21;
Matches   29; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

Qy   42 KRYTHGRGFITKAINSCHTSSLATPEDKE 70
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Db   63 KRYTHGRGFITKAINSCHTSSLATPEDKE 91

RESULT 4
Q8HXS1
ID   Q8HXS1   PRELIMINARY;   PRT;   229 AA.
AC   Q8HXS1;
DT   01-MAR-2003 (TrEMBLrel. 23, Created)
DT   01-MAR-2003 (TrEMBLrel. 23, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Prolaction precursor.
OS   Ailuropoda melanoleuca (Giant panda).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Ursidae; Ailuropoda.
OX   NCBI_TaxID=9646;
RN   [1]
RP   SEQUENCE FROM N.A.
RC   TISSUE=Pituitary;
RA   Zheng X., Zhu M., Zhang Z.;
RT   "Cloning and expression of pituitary prolactin gene in Ailuropoda
RT   melanoleuca.";
RL   Submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY161285; AAN78320.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
DR   InterPro; IPR001400; Somatotropin.
DR   Pfam; PF00103; hormone_1.
DR   PRINTS; PR00836; SOMATOTROPIN.
DR   PROSITE; PS00266; SOMATOTROPIN_1; 1.
DR   PROSITE; PS00338; SOMATOTROPIN_2; 1.
KW   Signal.
FT   SIGNAL   1   30   POTENTIAL.
SQ   SEQUENCE 229 AA; 26236 MW; 441E3D748CFDDBC2 CRC64;

Query Match   12.6%; Score 25; DB 6; Length 229;
Best Local Similarity   100.0%; Pred. No. 2.3e-17;
Matches   25; Conservative   0; Mismatches   0; Indels   0; Gaps   0;

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Db   199 YNLLHCLRRDSHKIDNYLKLLKCRI 223

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ID   Q864R8   PRELIMINARY;   PRT;   229 AA.
AC   Q864R8;
DT   01-JUN-2003 (TrEMBLrel. 24, Created)
DT   01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
DT   01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
DE   Preprolactin precursor.
OS   Mustela vison (American mink).
OC   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC   Mammalia; Eutheria; Carnivora; Fissipedia; Mustelidae; Mustelinae;
OC   Mustela.
OX   NCBI_TaxID=9667;
RN   [1]
RP   SEQUENCE FROM N.A.
RA   Vardy T.L., Farid A.;
RT   "Nucleotide sequence variation of the mink preprolactin gene.";
RL   Submitted (MAR-2003) to the EMBL/GenBank/DDBJ databases.
DR   EMBL; AY249860; AAO92934.1; -.
DR   GO; GO:0005576; C:extracellular; IEA.
DR   GO; GO:0005179; F:hormone activity; IEA.
DR   InterPro; IPR001400; Somatotropin.
DR   Pfam; PF00103; hormone_1.
DR   PRINTS; PR00836; SOMATOTROPIN.
DR   PROSITE; PS00266; SOMATOTROPIN_1; 1.
DR   PROSITE; PS00338; SOMATOTROPIN_2; 1.
KW   Signal.
FT   SIGNAL   1   30   Potential.
FT   CHAIN   31   70   prolactin.
FT   CHAIN   71   106   prolactin.

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                    GenCore version 5.1.6
          Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - protein search, using sw model

Run on:       September 13, 2004, 12:27:50 .; Search time 32 Seconds
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Title:        US-10-735-594-1
Perfect score: 199
Sequence:     1 LPICPGGAARCQVTLRDLFD.........HKIDNYLKLLKCRIIHNNNC 199

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              Gapop 60.0 , Gapext 60.0

Searched:     389414 seqs, 51625971 residues

Word size :   0

Total number of hits satisfying chosen parameters:        389414

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Listing first 45 summaries

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

                              SUMMARIES

Result          %   Query
No.    Score Match Length DB  ID                     Description
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  1     199  100.0  199    3  US-08-737-248-7        Sequence 7, Appli
  2     199  100.0  351    1  US-08-196-350-1        Sequence 1, Appli
  3      68   34.2  125    3  US-08-985-526-25       Sequence 25, Appl
  4      68   34.2  253    3  US-08-985-526-27       Sequence 27, Appl
  5      26   13.1  199    3  US-08-737-248-10       Sequence 10, Appl
  6      26   13.1  199    3  US-08-737-248-12       Sequence 12, Appl
  7      26   13.1  199    3  US-08-737-248-14       Sequence 14, Appl
  8      25   12.6  199    3  US-08-737-248-8        Sequence 8, Appli
  9      24   12.1  197    3  US-08-737-248-17       Sequence 17, Appl
 10      24   12.1  198    3  US-08-737-248-6        Sequence 6, Appli
 11      19    9.5  199    3  US-08-737-248-2        Sequence 2, Appli
 12      19    9.5  426    3  US-08-737-248-4        Sequence 4, Appli
 13      14    7.0  197    3  US-08-737-248-15       Sequence 15, Appl
 14      13    6.5  197    3  US-08-737-248-16       Sequence 16, Appl
 15      12    6.0  199    3  US-08-737-248-5        Sequence 5, Appli
 16      12    6.0  199    3  US-08-737-248-11       Sequence 11, Appl
 17      12    6.0  199    3  US-08-737-248-13       Sequence 13, Appl
 18      10    5.0  188    3  US-08-737-248-20       Sequence 20, Appl
 19      10    5.0  199    3  US-08-737-248-9        Sequence 9, Appli
 20       8    4.0    8    2  US-08-669-284B-28      Sequence 28, Appl
 21       8    4.0    8    3  US-09-190-964-13       Sequence 13, Appl
 22       8    4.0  177    3  US-08-737-248-21       Sequence 21, Appl
 23       8    4.0  187    3  US-08-737-248-18       Sequence 18, Appl
 24       8    4.0  187    3  US-08-737-248-19       Sequence 19, Appl
 25       7    3.5  163    4  US-09-252-991A-18617   Sequence 18617, A
 26       7    3.5  165    4  US-09-519-232-44       Sequence 44, Appl
 27       7    3.5  207    1  US-07-656-566-2        Sequence 2, Appli
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 28       7    3.5  212    4  US-09-134-000C-4518    Sequence 4518, Ap
 29       7    3.5  231    1  US-07-656-566-3        Sequence 3, Appli
 30       7    3.5  238    4  US-09-145-828A-13      Sequence 13, Appl
 31       7    3.5  238    4  US-09-903-456-20       Sequence 20, Appl
 32       7    3.5  301    1  US-08-393-985-12       Sequence 12, Appl
 33       7    3.5  347    1  US-08-118-270-47       Sequence 47, Appl
 34       7    3.5  347    5  PCT-US93-08528-47      Sequence 47, Appl
 35       7    3.5  369    2  US-08-951-148-8        Sequence 8, Appli
 36       7    3.5  369    2  US-09-165-234-8        Sequence 8, Appli
 37       7    3.5  369    3  US-09-274-570-8        Sequence 8, Appli
 38       7    3.5  466    4  US-09-489-039A-7654    Sequence 7654, Ap
 39       7    3.5  511    4  US-09-540-236-2979     Sequence 2979, Ap
 40       7    3.5  529    4  US-09-328-352-5413     Sequence 5413, Ap
 41       7    3.5  591    4  US-09-519-232-66       Sequence 66, Appl
 42       7    3.5  943    4  US-09-397-885-5        Sequence 5, Appli
 43       7    3.5  943    4  US-09-969-362-5        Sequence 5, Appli
 44       7    3.5 1305    4  US-08-864-785-3        Sequence 3, Appli
 45       7    3.5 1353    3  US-08-894-173-2        Sequence 2, Appli

                            ALIGNMENTS

RESULT 1
US-08-737-248-7
; Sequence 7, Application US/08737248
; Patent No. 6114305
; GENERAL INFORMATION:
;    APPLICANT: Guemene, Daniel
;    APPLICANT: Zadworny, David
;    APPLICANT: Karatzas, Costas
;    TITLE OF INVENTION: USE OF PROLACTIN FOR PREVENTING AND/OR
;    TITLE OF INVENTION: TREATING BIRD BROODINESS
;    NUMBER OF SEQUENCES: 23
;    CORRESPONDENCE ADDRESS:
;       ADDRESSEE: WEISER & ASSOCIATES
;       STREET: 230 South Fifteenth Street, Suite 500
;       CITY: Philadelphia
;       STATE: PA
;       COUNTRY: USA
;       ZIP: 19102
;    COMPUTER READABLE FORM:
;       MEDIUM TYPE: Floppy disk
;       COMPUTER: IBM PC compatible
;       OPERATING SYSTEM: PC-DOS/MS-DOS
;       SOFTWARE: PatentIn Release #1.0, Version #1.30
;    CURRENT APPLICATION DATA:
;       APPLICATION NUMBER: US/08/737,248
;       FILING DATE: 28-APR-1997
;       CLASSIFICATION: 424
;    PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: PCT/FR95/00576
;       FILING DATE: 03-MAY-1995
;    PRIOR APPLICATION DATA:
;       APPLICATION NUMBER: FR 94/05550
;       FILING DATE: 05-MAY-1994
;    ATTORNEY/AGENT INFORMATION:
;       NAME: Weiser, Gerard J.
;       REGISTRATION NUMBER: 19,763
;       REFERENCE/DOCKET NUMBER: 989.6411P
;    TELECOMMUNICATION INFORMATION:
;       TELEPHONE: 215-875-8383
;       TELEFAX: 215-875-8394
;    INFORMATION FOR SEQ ID NO: 7:
;       SEQUENCE CHARACTERISTICS:
;          LENGTH: 199 amino acids
;          TYPE: amino acid
;          STRANDEDNESS:
;          TOPOLOGY: linear
;       MOLECULE TYPE: protein
US-08-737-248-7

Query Match             100.0%;  Score 199;  DB 3;  Length 199;
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Matches 199;   Conservative   0;   Mismatches   0;   Indels   0;   Gaps   0;

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Qy   61 SSLATPEDKEQAQQMNQKDFLSLIVSILRSWNEPLYHLVTEVRGMQEAPEAILSKAVEIE 120
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Qy  121 EQTKRLLEGMELIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSH 180
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Db  121 EQTKRLLEGMELIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSH 180

Qy  181 KIDNYLKLLKCRIIHNNNC 199
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Db  181 KIDNYLKLLKCRIIHNNNC 199
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RESULT 2
US-08-196-350-1
; Sequence 1, Application US/08196350
; Patent No. 5585099
; GENERAL INFORMATION:
;   APPLICANT: Richards, Sue
;   APPLICANT: Kaplan, Joanne
;   APPLICANT: Moscicki, Richard
;   TITLE OF INVENTION: PROLACTIN AS ADJUVANT
;   NUMBER OF SEQUENCES: 2
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Brad Salcedo
;   STREET: One Kendall Square
;   CITY: Cambridge
;   STATE: MA
;   COUNTRY: U.S.A.
;   ZIP: 02139
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/196,350
;   FILING DATE:
;   CLASSIFICATION: 424
;   ATTORNEY/AGENT INFORMATION:
;   NAME: Gosz, William G
;   REGISTRATION NUMBER: 27,787
;   REFERENCE/DOCKET NUMBER: GEN 4-1.0
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 6172527868
;   TELEFAX: 6173747225
; INFORMATION FOR SEQ ID NO: 1:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 351 amino acids
;   TYPE: amino acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   MOLECULE TYPE: peptide
;   ANTI-SENSE: NO
;   FRAGMENT TYPE: N-terminal
;   ORIGINAL SOURCE:
;   ORGANISM: human prolactin
US-08-196-350-1

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Qy  121 EQTKRLLEGMELIVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSH 180
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Qy  181 KIDNYLKLLKCRIIHNNNC 199
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Db  333 KIDNYLKLLKCRIIHNNNC 351
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RESULT 3
US-08-985-526-25
; Sequence 25, Application US/08985526
; Patent No. 6080728
; GENERAL INFORMATION:
;   APPLICANT: Mixson, James A
;   TITLE OF INVENTION: CARRIER:DNA COMPLEXES CONTAINING DNA
;   TITLE OF INVENTION: ENCODING ANTI-ANGIOGENIC PEPTIDES AND THEIR USE IN GENE
;   TITLE OF INVENTION: THERAPY
;   NUMBER OF SEQUENCES: 43
;   CORRESPONDENCE ADDRESS:
;   ADDRESSEE: Connolly, Bove, Lodge, & Hutz
;   STREET: 1220 Market Street, P.O. Box 2207
;   CITY: Wilmington
;   STATE: Delaware
;   COUNTRY: U.S.A.
;   ZIP: 19899
;   COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/985,526
;   FILING DATE:
;   CLASSIFICATION:
;   PRIOR APPLICATION DATA:
;   APPLICATION NUMBER: US 08/608,845
;   FILING DATE: 16-JUL-1996
;   ATTORNEY/AGENT INFORMATION:
;   NAME: McMorrow Jr., Robert G
;   TELECOMMUNICATION INFORMATION:
;   TELEPHONE: (302) 658-9141
;   TELEFAX: (302) 658-5613
; INFORMATION FOR SEQ ID NO: 25:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 125 amino acids
;   TYPE: amino acid
;   TOPOLOGY: linear
;
US-08-985-526-25

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Query Match       34.2%;   Score 68;   DB 3;   Length 125;
Best Local Similarity  100.0%;   Pred. No. 1.2e-60;
Matches 68;   Conservative  0;   Mismatches  0;   Indels  0;   Gaps  0;

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Db   43 KRYTHGRGFITKAINSCHTSSLATPEDKEQAQQMNQKDFLSLIVSILRSWNEPLYHLVTE 102

Qy  102 VRGMQEAP 109
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Db  103 VRGMQEAP 110
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RESULT 4
US-08-985-526-27
; Sequence 27, Application US/08985526
; Patent No. 6080728
; GENERAL INFORMATION:

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        Copyright (c) 1993 - 2004 Compugen Ltd.

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                 Delop   6.0 , Delext   7.0

Searched:        3470272 seqs, 2167516995 residues

Total number of hits satisfying chosen parameters:      6940544

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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-DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :    GenEmbl:*
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         2:   gb_htg:*           30:  em_htg_hum:*
         3:   gb_in:*            31:  em_htg_inv:*
         4:   gb_om:*            32:  em_htg_other:*
         5:   gb_ov:*            33:  em_htg_mus:*
         6:   gb_pat:*           34:  em_htg_pln:*
         7:   gb_ph:*            35:  em_htg_rod:*
         8:   gb_pl:*            36:  em_htg_mam:*
         9:   gb_pr:*            37:  em_htg_vrt:*
        10:   gb_ro:*            38:  em_sy:*
        11:   gb_sts:*           39:  em_htgo_hum:*
        12:   gb_sy:*            40:  em_htgo_mus:*
        13:   gb_un:*            41:  em_htgo_other:*
        14:   gb_vi:*
        15:   em_ba:*
        16:   em_fun:*
        17:   em_hum:*
        18:   em_in:*
        19:   em_mu:*
        20:   em_om:*
        21:   em_or:*
        22:   em_ov:*
        23:   em_pat:*
        24:   em_ph:*
        25:   em_pl:*
        26:   em_ro:*
        27:   em_sts:*
        28:   em_un:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1043	100.0	833	6	AX587623	AX587623 Sequence
2	1043	100.0	833	9	HSLACT	V00566 Homo sapien
3	1043	100.0	960	6	E02152	E02152 DNA encodin
4	1043	100.0	970	6	AR270853	AR270853 Sequence
5	1043	100.0	970	6	HSPRO205	X54393 H.sapiens m
6	1043	100.0	1071	6	AX014109	AX014109 Sequence
7	1043	100.0	1071	6	BD204679	BD204679 Human nuc
8	1043	100.0	1100	9	I31987	I31987 Sequence 2
9	1043	100.0	1388	9	BC015850	BC015850 Homo sapi
10	1043	100.0	3541	6	E00953	E00953 Plasmid for
11	1036	99.3	807	9	HUMPRLA	M29386 Human prola
12	1036	99.3	5278	6	E02430	E02430 DNA encodin
13	1033	99.0	807	9	HUMPRLD	D00411 Homo sapien
14	1020	97.8	1150	9	MMU09018	U09018 Macaca mula
15	885	84.9	574	9	HSU75583	U75583 Homo sapien
16	879	84.3	868	4	AY373339	AY373339 Equus cab
17	878	84.2	690	4	AY161285	AY161285 Equus cab
18	877	84.1	841	4	SSPPLAC	X14068 Porcine mRN
19	874	83.8	880	4	OCU27199	U27199 Oryctolagus
20	867	83.1	884	4	FCU25974	U25974 Felis catus
21	857	82.2	862	4	AF054634	AF054634 Trichosur
22	852	81.7	713	4	MVRNAP	X59785 M.vison gen
23	847	81.2	854	4	AF067726	AF067726 Monodelph
24	838	80.3	892	3	THY457817	AJ457817 Taenia hy
25	803	77.0	864	4	AY373035	AY373035 Cervus el
26	798	76.5	847	4	CHCPRNA	X76049 C.hircus ca
27	797	76.4	907	4	BTLACT	V00112 Bos taurus
28	797	76.4	3549	6	E00955	E00955 Plasmid for
29	796	76.3	847	4	CHMGP1	X76048 C.hircus ca
30	796	76.3	880	4	OALHR	X13483 Sheep mRNA
31	794	76.1	926	4	SHPPRL	M27057 Ovine prola
32	790	75.7	847	4	OAMGMRNA	X76050 O.aries ovi
33	772	74.0	682	4	MVPROLAC	X63235 Mustela vis
34	754	72.3	600	6	A47306	A47306 Sequence 1
35	754	72.3	600	6	AR110193	AR110193 Sequence
36	754	72.3	924	5	MGPLAC	X51769 Turkey mRNA
37	754	72.3	1281	6	A47307	A47307 Sequence 2
38	754	72.3	1281	6	AR110194	AR110194 Sequence
39	752	72.1	702	5	AY332494	AY332494 Ambystoma
40	748	71.7	953	5	CHKPRL	J04614 Chicken pro
41	748	71.7	953	5	MGU05952	U05952 Meleagris g
42	748	71.7	978	6	E02259	E02259 cDNA encodi
43	701	67.2	908	5	XELPRL	L07620 Frog prolac
44	690.5	66.2	899	5	RCPROLACT	X16063 R.cartesbei
45	667	64.0	900	6	E03099	E03099 DNA encodin

ALIGNMENTS

RESULT 1

RESULT 1

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AX587623
LOCUS       AX587623                 833 bp    DNA     linear   PAT 10-JAN-2003
DEFINITION  Sequence 93 from Patent WO0246467.
ACCESSION   AX587623
VERSION     AX587623.1  GI:28212349
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bertucci,F., Houlgatte,R., Birnbaum,D., Nguyen,C., Viens,P. and
            Fert,V.
  TITLE     Gene expression profiling of primary breast carcinomas using arrays
            of candidate genes
  JOURNAL   Patent: WO 0246467-A 93 13-JUN-2002;
            Ipsogen (FR)
FEATURES             Location/Qualifiers
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                     /note="prolactin (PRL) gene."
ORIGIN

Alignment Scores:
Pred. No.:              4.43e-98          Length:       833
Score:                  1043.00          Matches:      199
Percent Similarity:     100.00%          Conservative:   0
Best Local Similarity:  100.00%          Mismatches:     0
Query Match:            100.00%          Indels:         0
DB:                     6                Gaps:           0

US-10-735-594-1 (1-199) x AX587623 (1-833)

Qy    1 LeuProIleCysProGlyGlyAlaAlaArgCysGlnValThrLeuArgAspLeuPheAsp 20
Db   89 TTGCCCATCTGTCCCGGCGGGGCTGCCCGATGCCAGGTGACCCTTCGAGACCTGTTTGAC 148

Qy   21 ArgAlaAlaValLeuSerHisTyrIleHisAsnLeuSerSerGluMetPheSerGluPhe 40
Db  149 CGCGCCGCTGTCCTGTCCCACTACATCCATAACCTCTCCTCAGAAATGTTCAGCGAATTC 208

Qy   41 AspLysArgTyrThrHisGlyAlaArgGlyPheIleThrLysAlaIleAsnSerCysHisThr 60
Db  209 GATAAACCGTATACCCATGGCCGGGGGTTCATTACCAAGGCCATCAACAGCTGCCACACT 268

Qy   61 SerSerLeuAlaThrProGluAspLysGlnAlaGlnGlnMetAsnGlnLysAspPhe 80
Db  269 TCTTCCCTTGCCACCCCCGAAGACAAGGAGCAAGCCCAACAGATGAATCAAAAAGACTTT 328

Qy   81 LeuSerLeuIleValSerIleLeuArgSerTrpAsnGluProLeuTyrHisLeuValThr 100
Db  329 CTGAGCCTGATAGTGAGCATATTGCGATCCTGGAATGAGCCTCTGTATCATCTGGTCACG 388

Qy  101 GluValArgGlyMetGlnGluAlaProGluAlaIleLeuSerLysAlaValGluIleGlu 120
Db  389 GAAGTACGTGGTATGCAAGAAGCCCCGGAAGCTATCCTATCCAAAGCTGTAGAGATTGAG 448

Qy  121 GlnThrLysArgLeuLeuGluGlyMetGluLeuIleValSerGlnValHisProGlu 140
Db  449 GAGCAAACCAAACGGCTTCTAGAGGGCATGGAGCTGATAGTGAGCCAGGTTCATCCTGAA 508

Qy  141 ThrLysGluAsnGluIleTyrProValTrpSerGlyLeuProSerLeuGlnMetAlaAsp 160
Db  509 ACCAAAGAAAATGAGATCTACCCTGTCTGGTCGGGACTTCCATCCCTCCAGATGGCTGAT 568

Qy  161 GluGluSerArgLeuSerAlaTyrTyrAsnLeuLeuHisCysLeuArgArgAspSerHis 180
Db  569 GAAGAGTCTCGCCTTTCTGCTTATTATAACCTGCTCCACTGCCTACGCAGGGATTCACAT 628

Qy  181 LysIleAspAsnTyrLeuLysLeuLeuLysCysArgIleIleHisAsnAsnCys 199
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Db  629 AAAATGACAATTATCTCAAGCTCCTGAAGTGCCGAATCATCCACAACAACACTGC 685

RESULT 2
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LOCUS       HSLACT                   833 bp    mRNA    linear   PRI 21-OCT-2003
DEFINITION  Homo sapiens mRNA for prolactin.
ACCESSION   V00566 J00299
VERSION     V00566.1  GI:34210
KEYWORDS    prolactin.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 833)
  AUTHORS   Cooke,N.E., Coit,D., Shine,J., Baxter,J.D. and Martial,J.A.
  TITLE     Human prolactin. cDNA structural analysis and evolutionary
            comparisons
  JOURNAL   J. Biol. Chem. 256 (8), 4007-4016 (1981)
  MEDLINE   81168179
   PUBMED   6260780
COMMENT     On Sep 5, 2003 this sequence version replaced gi:190353.
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                     /mol_type="mRNA"
                     /db_xref="taxon:9606"
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     CDS             5..688
                     /codon_start=1
                     /product="prolactin"
                     /protein_id="CAA23829.1"
                     /db_xref="GI:34211"
                     /db_xref="GOA:P01236"
                     /db_xref="SWISS-PROT:P01236"
                     /translation="MNIKGSPWKGSLLLLVSNLLLCQSVAPLPICPGGAARCQVTLR
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                     IVSQVHPETKENEIYPVWSGLPSLQMADEESRLSAYYNLLHCLRRDSHKIDNYLKLLK
                     CRIIHNNNC"

ORIGIN

Alignment Scores:
Pred. No.:              4.43e-98          Length:       833
Score:                  1043.00          Matches:      199
Percent Similarity:     100.00%          Conservative:   0
Best Local Similarity:  100.00%          Mismatches:     0
Query Match:            100.00%          Indels:         0
DB:                     9                Gaps:           0

US-10-735-594-1 (1-199) x HSLACT (1-833)

Qy    1 LeuProIleCysProGlyGlyAlaAlaArgCysGlnValThrLeuArgAspLeuPheAsp 20
Db   89 TTGCCCATCTGTCCCGGCGGGGCTGCCCGATGCCAGGTGACCCTTCGAGACCTGTTTGAC 148

Qy   21 ArgAlaAlaValLeuSerHisTyrIleHisAsnLeuSerSerGluMetPheSerGluPhe 40
Db  149 CGCGCCGCTGTCCTGTCCCACTACATCCATAACCTCTCCTCAGAAATGTTCAGCGAATTC 208

Qy   41 AspLysArgTyrThrHisGlyAlaArgGlyPheIleThrLysAlaIleAsnSerCysHisThr 60
Db  209 GATAAACCGTATACCCATGGCCGGGGGTTCATTACCAAGGCCATCAACAGCTGCCACACT 268

Qy   61 SerSerLeuAlaThrProGluAspLysGlnAlaGlnGlnMetAsnGlnLysAspPhe 80
Db  269 TCTTCCCTTGCCACCCCCGAAGACAAGGAGCAAGCCCAACAGATGAATCAAAAAGACTTT 328

Qy   81 LeuSerLeuIleValSerIleLeuArgSerTrpAsnGluProLeuTyrHisLeuValThr 100
Db  329 CTGAGCCTGATAGTGAGCATATTGCGATCCTGGAATGAGCCTCTGTATCATCTGGTCACG 388
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OM protein - nucleic search, using frame_plus_p2n model

Run on: September 13, 2004, 15:00:54 ; Search time 2733 Seconds
                                               (without alignments)
                                               2174.378 Million cell updates/sec

Title: US-10-735-594-1
Perfect score: 1043
Sequence: 1 LPICPGGAARCQVTLRDLFD.........HKIDNYLKLLKCRIIHNNNC 199

Scoring table: BLOSUM62
               Xgapop 10.0 , Xgapext 0.5
               Ygapop 10.0 , Ygapext 0.5
               Fgapop   6.0 , Fgapext 7.0
               Delop   6.0 , Delext   7.0

Searched: 27513289 seqs, 14931090276 residues

Total number of hits satisfying chosen parameters: 55026578

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

Command line parameters:
 -MODEL=frame+_p2n.model -DEV=xlp
 -Q=/cgn2_1/USPTO_spool_p/US10735594/runat_10092004_144654_5565/app_query.fasta_1.391
 -DB=EST -QFMT=fastap -SUFFIX=p2n.rst -MINMATCH=0.1 -LOOPCL=0 -LOOPEXT=0
 -UNITS=bits -START=1 -END=-1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45
 -DOCALIGN=200 -THR_SCORE=pct -THR_MAX=100 -THR_MIN=0 -ALIGN=15 -MODE=LOCAL
 -OUTFMT=pto -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
 -USER=US10735594 @CGN_1_1_6425 @runat_10092004_144654_5565 -NCPU=6 -ICPU=3
 -NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
 -DEV_TIMEOUT=120 -WARN_TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6
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          16: em_estom:*
          17: em_gss_hum:*
          18: em_gss_inv:*
          19: em_gss_pln:*
          20: em_gss_vrt:*
          21: em_gss_fun:*
          22: em_gss_mam:*
          23: em_gss_mus:*
          24: em_gss_pro:*
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          28: gb_gss1:*
          29: gb_gss2:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query Match	Length	DB	ID	Description
1	1043	100.0	740	14	CD239100	CD239100 FNPBKE08
2	1043	100.0	741	14	CD239111	CD239111 FNPBKF09
3	1043	100.0	747	14	CD239635	CD239635 FNPBWG10
4	1043	100.0	749	14	CD239093	CD239093 FNPBKD11
5	1043	100.0	749	14	CD239460	CD239460 FNPBUG08
6	1043	100.0	764	14	CD519470	CD519470 AGENCOURT
7	1043	100.0	810	14	CD251429	CD251429 AGENCOURT
8	1043	100.0	813	14	CD251266	CD251266 AGENCOURT
9	1043	100.0	816	14	CD106943	CD106943 AGENCOURT
10	1043	100.0	821	14	CD106883	CD106883 AGENCOURT
11	1043	100.0	821	14	CD251609	CD251609 AGENCOURT
12	1043	100.0	823	14	CD107449	CD107449 AGENCOURT
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14	1043	100.0	826	14	CD108217	CD108217 AGENCOURT
15	1043	100.0	826	14	CD251270	CD251270 AGENCOURT
16	1043	100.0	827	14	CD106496	CD106496 AGENCOURT
17	1043	100.0	831	14	CD107309	CD107309 AGENCOURT
18	1043	100.0	831	14	CD107478	CD107478 AGENCOURT
19	1043	100.0	833	14	CD108227	CD108227 AGENCOURT
20	1043	100.0	833	14	CD109012	CD109012 AGENCOURT
21	1043	100.0	834	14	CD109196	CD109196 AGENCOURT
22	1043	100.0	836	14	CD107815	CD107815 AGENCOURT
23	1043	100.0	836	14	CD108115	CD108115 AGENCOURT
24	1043	100.0	837	14	CD251598	CD251598 AGENCOURT
25	1043	100.0	838	14	CD107678	CD107678 AGENCOURT
26	1043	100.0	838	14	CD108894	CD108894 AGENCOURT
27	1043	100.0	840	14	CD108216	CD108216 AGENCOURT
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29	1043	100.0	843	14	CD108102	CD108102 AGENCOURT
30	1043	100.0	844	14	CD108091	CD108091 AGENCOURT
31	1043	100.0	844	14	CD108225	CD108225 AGENCOURT
32	1043	100.0	844	14	CD513187	CD513187 AGENCOURT
33	1043	100.0	846	14	CD107688	CD107688 AGENCOURT
34	1043	100.0	846	14	CD108472	CD108472 AGENCOURT
35	1043	100.0	846	14	CD108933	CD108933 AGENCOURT
36	1043	100.0	847	14	CD106099	CD106099 AGENCOURT
37	1043	100.0	849	14	CD251113	CD251113 AGENCOURT
38	1043	100.0	849	14	CD513048	CD513048 AGENCOURT
39	1043	100.0	851	14	CD105722	CD105722 AGENCOURT
40	1043	100.0	851	14	CD106918	CD106918 AGENCOURT
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42	1043	100.0	851	14	CD108633	CD108633 AGENCOURT
43	1043	100.0	852	14	CD106017	CD106017 AGENCOURT
44	1043	100.0	852	14	CD106785	CD106785 AGENCOURT
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ALIGNMENTS

RESULT 1
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LOCUS   CD239100   740 bp   mRNA   linear   EST 21-MAY-2003
DEFINITION   FNPBKE08 FNP Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD239100
VERSION   CD239100.1 GI:30982565
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM   Homo sapiens
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             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 740)
AUTHORS   Ma,Y., Qi,X., Zhang,X., Xiao,H., Zhu,Z., Yan,Q., Chen,Z. and Han,Z.

Wed Sep 15 08:30:10 2004   us-10-735-594-1.p2n.rst

TITLE   Fetal Pituitary ESTs
JOURNAL   Unpublished (2003)
COMMENT   Contact: Zeguang Han
           Chinese National Human Genome Center at Shanghai
           351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
           201203, P. R. China
           Tel: 86-21-50801919(ex.45)
           Fax: 86-21-50801922
           Email: hanzg@chgc.sh.cn.
FEATURES   Location/Qualifiers
     source   1..740
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                     /db_xref="taxon:9606"
                     /tissue_type="pituitary"
                     /dev_stage="fetal"
                     /clone_lib="FNP"
                     /note="Vector: pTriplEx2; Site_1: sfiIA; Site_2: sfiIBl"

ORIGIN

Alignment Scores:
Pred. No.:   4.15e-116   Length: 740
Score: 1043.00   Matches: 199
Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
DB: Gaps: 14

US-10-735-594-1 (1-199) x CD239100 (1-740)

Qy   1 LeuProIleCysProGlyGlyAlaAlaArgCysGlnValThrLeuArgAspLeuPheAsp 20
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Db   136 TTGCCCATCTGTCCCGGCGGTGCCGCCCGGTGCCCAGGTGACCCTTCGAGACCTGTTTGAC 195

Qy   21 ArgAlaAlaValLeuSerHisTyrIleHisAsnLeuSerGluMetPheSerGluPhe 40
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   41 AspLysArgTyrThrHisGlyArgGlyPheIleThrLysAlaIleAsnSerCysHisThr 60
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Qy   61 SerSerLeuAlaThrProGluAspLysGlnAlaGlnMetAsnGlnLysAspPhe 80
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   316 TCTTCCCTTGCCACCCCAGAGAGACAAGGCAAGCCCACAGATGAATCAAAAAGACTTT 375

Qy   81 LeuSerLeuIleValSerIleLeuArgSerTrpAsnGluProLeuTyrHisLeuValThr 100
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   376 CTGAGCCTGATAGTCAGCATATTGCGATCCTGGAATGAGCCTCTGTATCATCTGGTCACG 435

Qy   101 GluValArgGlyMetGlnGluAlaProGluAlaIleLeuSerLysAlaValGluIleGlu 120
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   436 GAAGTACGTGGTATGCAAGAAGCCCCGGAGGCTATCCTATCCAAAGCTGTAGAGATTGAG 495

Qy   121 GluGlnThrLysArgLeuLeuGlyMetGluLeuValSerGlnValHisProGlu 140
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   496 GAGCAAACCAAACGGCTTCTAGGGATGGAGCTGGTGAGTCAGGTTCATCCTGAA 555

Qy   141 ThrLysAsnGluIleTyrProValTrpSerGlyLeuProSerLeuGlnMetAlaAsp 160
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Qy   161 GluGluSerArgLeuSerAlaTyrTyrAsnLeuLeuHisCysLeuArgArgAspSerHis 180
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
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Qy   181 LysIleAspAsnTyrLeuLysLeuLeuLysCysArgIleHisAsnAsnAsnCys 199
            |||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   676 AAAATCGACAATTATCTCAAGCTCCTGAAGTGCCGAATCCATAACAACAACTGC 732

RESULT 2
CD239111
LOCUS   CD239111   741 bp   mRNA   linear   EST 21-MAY-2003
DEFINITION FNPBKF09 FNP Homo sapiens cDNA, mRNA sequence.
ACCESSION   CD239111
VERSION   CD239111.1   GI:30982576
KEYWORDS   EST.
SOURCE   Homo sapiens (human)
  ORGANISM Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1 (bases 1 to 741)
  AUTHORS   Ma,Y., Qi,X., Zhang,X., Xiao,H., Zhu,Z., Yan,Q., Chen,Z., and Han,Z.
  TITLE   Fetal Pituitary ESTs
  JOURNAL   Unpublished (2003)
COMMENT   Contact: Zeguang Han
            Chinese National Human Genome Center at Shanghai
            351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
            201203, P. R. China
            Tel: 86-21-50801919(ex.45)
            Fax: 86-21-50801922
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Percent Similarity: 100.00%   Conservative: 0
Best Local Similarity: 100.00%   Mismatches: 0
Query Match: 100.00%   Indels: 0
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US-10-735-594-1 (1-199) x CD239111 (1-741)

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Db   138 TTGCCCATCTGTCCCGGCGGTGCCGCCCGGTGCCCAGGTGACCCTTCGAGACCTGTTTGAC 197

Qy   21 ArgAlaAlaValLeuSerHisTyrIleHisAsnLeuSerGluMetPheSerGluPhe 40
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Db   198 CGCGCCGTGCTCGTGTCCCACTACATCCATAACCTCTCCCAGAAATGTTCAGCGAATTC 257

Qy   41 AspLysArgTyrThrHisGlyArgGlyPheIleThrLysAlaIleAsnSerCysHisThr 60
            |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   258 GATAAACGGTATACCCATGGCCGGGGGTTCATTACCAAGGCCATCAACAGCTGCCACACT 317

Qy   61 SerSerLeuAlaThrProGluAspLysGlnAlaGlnMetAsnGlnLysAspPhe 80
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Qy   81 LeuSerLeuIleValSerIleLeuArgSerTrpAsnGluProLeuTyrHisLeuValThr 100
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Qy   101 GluValArgGlyMetGlnGluAlaProGluAlaIleLeuSerLysAlaValGluIleGlu 120
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Qy   161 GluGluSerArgLeuSerAlaTyrTyrAsnLeuLeuHisCysLeuArgArgAspSerHis 180

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                    GenCore version 5.1.6
              Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:     September 13, 2004, 16:02:14 ; Search time 80 Seconds
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Post-processing: Minimum Match 0%
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Pred. No. is the number of results predicted by chance to have a
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                                SUMMARIES

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6	641	61.5	771	3	US-08-985-526-28	Sequence 28, Appl
7	263	25.2	933	3	US-09-602-848-1	Sequence 1, Appli
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24	184	17.6	596	4	US-07-826-928A-29	Sequence 29, Appl
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; Sequence 1416, Application US/09016434
; Patent No. 5514646-37
; GENERAL INFORMATION:
;  APPLICANT: Janice Au-Young
;  TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
;  TITLE OF INVENTION: PATHWAY GENE EXPRESSION
;  NUMBER OF SEQUENCES: 1490
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
;  STREET: 3174 PORTER DRIVE
;  CITY: PALO ALTO
;  STATE: CALIFORNIA
;  COUNTRY: USA
;  ZIP: 94304
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE: Floppy disk
;  COMPUTER: IBM PC compatible
;  OPERATING SYSTEM: PC-DOS/MS-DOS
;  SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/09/016,434
;  FILING DATE: HEREWITH
;  CLASSIFICATION:
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER:
;  FILING DATE:
;  CLASSIFICATION:
;  ATTORNEY/AGENT INFORMATION:
;  NAME: Zeller, Karen J.
;  REGISTRATION NUMBER: 37,071
;  REFERENCE/DOCKET NUMBER: PA-0002 US
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE: (650) 855-0555
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;      TELEFAX:   (650) 845-4166
; INFORMATION FOR SEQ ID NO:   1416:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:   970 base pairs
;      TYPE:   nucleic acid
;      STRANDEDNESS:   single
;      TOPOLOGY:   linear
;      IMMEDIATE SOURCE:
;        LIBRARY:   GENBANK
;        CLONE:   g531102
US-09-016-434-1416

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RESULT 2
US-08-196-350-2
; Sequence 2, Application US/08196350
; Patent No. 5585099
; GENERAL INFORMATION:
;    APPLICANT:   Richards, Sue
;    APPLICANT:   Kaplan, Joanne
;    APPLICANT:   Moscicki, Richard
;    TITLE OF INVENTION:   PROLACTIN AS ADUVANT
;    NUMBER OF SEQUENCES:   2
;    CORRESPONDENCE ADDRESS:
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;      ADDRESSEE:   Brad Salcedo
;      STREET:   One Kendall Square
;      CITY:   Cambridge
;      STATE:   MA
;      COUNTRY:   U.S.A.
;      ZIP:   02139
;   COMPUTER READABLE FORM:
;      MEDIUM TYPE:   Floppy disk
;      COMPUTER:   IBM PC compatible
;      OPERATING SYSTEM:   PC-DOS/MS-DOS
;      SOFTWARE:   PatentIn Release #1.0, Version #1.25
;   CURRENT APPLICATION DATA:
;      APPLICATION NUMBER:   US/08/196,350
;      FILING DATE:
;      CLASSIFICATION:   424
;   ATTORNEY/AGENT INFORMATION:
;      NAME:   Gosz, William G
;      REGISTRATION NUMBER:   27,787
;      REFERENCE/DOCKET NUMBER:   GEN 4-1.0
;   TELECOMMUNICATION INFORMATION:
;      TELEPHONE:   6172527868
;      TELEFAX:   6173744225
; INFORMATION FOR SEQ ID NO:   2:
;      SEQUENCE CHARACTERISTICS:
;      LENGTH:   1100 base pairs
;      TYPE:   nucleic acid
;      STRANDEDNESS:   single
;      TOPOLOGY:   linear
;      MOLECULE TYPE:   cDNA
US-08-196-350-2

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Qy   21 ArgAlaValValLeuSerHisTyrIleHisAsnLeuSerGluMetPheSerGluPhe  40
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Qy   61 SerSerLeuAlaThrProGluAspLysGlyGlnAlaGlnMetAsnGlnLysAspPhe  80
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Qy   81 LeuSerLeuIleValSerIleLeuArgSerTrpAsnGluProLeuTyrHisLeuValThr 100
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OM protein - nucleic search, using frame_plus_p2n model

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                Copyright  (c) 1993 - 2004  Compugen Ltd.

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Run on:         September 13, 2004, 18:16:39 ; Search time 4226 Seconds
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Searched:       3470272 seqs, 2167151516995 residues

Word size:      1

Total number of hits satisfying chosen parameters:        6934743

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-NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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SUMMARIES

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

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4	199	100.0	970	6	AR270853	AR270853 Sequence
5	199	100.0	970	9	HSPRO205	X54393 H.sapiens m
6	199	100.0	1071	6	AX014109	AX014109 Sequence
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9	199	100.0	1388	6	BC015850	BC015850 Homo sapi
10	199	100.0	3541	6	E00953	E00953 Plasmid for
11	185	93.0	5278	6	E02430	E02430 DNA encodin
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16	124	62.3	387	6	E34067	E34067 Carrier/DNA
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31	26	13.1	841	4	SSPPLAC	X14068 Porcine mRN
32	26	13.1	880	4	OCU27199	U27199 Oryctolagus
33	25	12.6	682	4	MVPROLAC	X63235 Mustela vis
34	25	12.6	690	4	AY161285	AY161285 Ailuropod
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42	24	12.1	908	5	XELPRL	L07620 Frog prolac
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ALIGNMENTS

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DEFINITION  Sequence 93 from Patent WO0246467.
ACCESSION   AX587623
VERSION     AX587623.1  GI:28212349
KEYWORDS    .
SOURCE      synthetic construct
  ORGANISM  synthetic construct
            artificial sequences.
REFERENCE   1
  AUTHORS   Bertucci,F., Houlgatte,R., Birnbaum,D., Nguyen,C., Viens,P. and
            Fert,V.
  TITLE     Gene expression profiling of primary breast carcinomas using arrays
            of candidate genes
  JOURNAL   Patent: WO 0246467-A 93 13-JUN-2002;
            Ipsogen (FR)
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US-10-735-594-1 (1-199) x AX587623 (1-833)

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Qy   81 LeuSerLeuIleValSerIleLeuArgSerTrpAsnGluProLeuTyrHisLeuValThr 100
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Qy  121 GluGlnThrLysArgLeuLeuGluGlyMetGluLeuIleValSerGlnValHisProGlu 140
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Qy  141 ThrLysGluAspAsnGluIleTyrProValTrpSerGlyLeuProSerLeuGlnMetAlaAsp 160
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DEFINITION  Homo sapiens mRNA for prolactin.
ACCESSION   V00566 J00299
VERSION     V00566.1  GI:34210
KEYWORDS    prolactin.
SOURCE      Homo sapiens (human)
  ORGANISM  Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1  (bases 1 to 833)
  AUTHORS   Cooke,N.E., Coit,D., Shine,J., Baxter,J.D. and Martial,J.A.
  TITLE     Human prolactin. cDNA structural analysis and evolutionary
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  JOURNAL   J. Biol. Chem. 256 (8), 4007-4016 (1981)
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ORIGIN

Alignment Scores:
Pred. No.:
Score:                  1.81e-198      Length:        833
Percent Similarity:     199.00         Matches:       199
Best Local Similarity:  100.00%        Conservative:  0
Query Match:            100.00%        Mismatches:    0
DB:                     .688           Indels:        0
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US-10-735-594-1 (1-199) x HSLACT (1-833)

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          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   89 TTGCCCATCTGTCCCGGCGGCGTGCCCGCTCGCCAGGTGACCCTTCGAGACCCTGTTTGAC 148

Qy   21 ArgAlaAlaValLeuSerHisTyrIleHisAsnLeuSerSerGluMetPheSerGluPhe 40
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  149 CGCGCCGTCGTCCTGTCCCACTACATCCATAACCTCTCCTCAGAAATGTTCAGCGAATTC 208

Qy   41 AspLysArgTyrHisGlyArgGlyPheIleThrLysAlaIleAsnSerCysHisThr 60
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Db  209 GATAAACGGTATCATGGCCGGGGGTTCATTACCAAGGCCATCAACAGCTGCCACACT 268

Qy   61 SerSerAlaThrProGluAspLysGlnValAlaGlnAlaArgCys... 80
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  269 TCTTCCCTTGCTCCACCCGAAGACAAGCAAGAGCAAGCCCAACAAGCCCAACAGTCAACCTTT 328

Qy   81 LeuSerLeuLeuValSerIleLeuArgSerTrpAsnGluProLeuTyrHisLeuValThr 100
          |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  329 CTGAGCCTGATAGTCAGCATATTGCGATCCTGGAATGAGCCCCTGTATCATCTGGTCACG 388
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OM protein - nucleic search, using frame_plus_p2n model

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　　　　　　　GenCore version 5.1.6
　　　　Copyright (c) 1993 - 2004 Compugen Ltd.
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Searched:　　　27513289 seqs, 1493109276 residues

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Total number of hits satisfying chosen parameters:　55025477

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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ACCESSION　　CD239100
VERSION　　　CD239100.1 GI:30982565
KEYWORDS　　EST.
SOURCE　　　Homo sapiens (human)
　ORGANISM　Homo sapiens
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　　　　　　Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE　　1　(bases 1 to 740)
AUTHORS　　Ma,Y., Qi,X., Zhang,X., Xiao,H., Zhu,Z., Yan,Q., Chen,Z. and Han,Z.

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ACCESSION    CD239111
VERSION      CD239111.1  GI:30982576
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SOURCE       Homo sapiens (human)
  ORGANISM   Homo sapiens
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             Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE    1 (bases 1 to 741)
  AUTHORS    Ma,Y., Qi,X., Zhang,X., Xiao,H., Zhu,Z., Yan,Q., Chen,Z. and Han,Z.
  TITLE      Fetal Pituitary ESTs
  JOURNAL    Unpublished (2003)
COMMENT      Contact: Zeguang Han
             Chinese National Human Genome Center at Shanghai
             351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
             201203, P. R. China
             Tel: 86-21-50801919(ex.45)
             Fax: 86-21-50801922
             Email: hanzg@chgc.sh.cn.
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ORIGIN

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US-10-735-594-1 (1-199) x CD239111 (1-741)

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US-10-735-594-1 (1-199) x CD239100 (1-740)

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Db   436 GAAGTACGTGGTATGCAAGCAGCCCCGGAGGCTATCCTATCCAAAGCTGTAGAAGATTGAG 495

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Qy   141 ThrLysGluAsnGluIleTyrProValTrpSerGlyLeuProSerLeuGlnMetAlaAsp 160
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Qy   161 GluGluSerArgLeuSerAlaTyrTyrAsnLeuHisCysLeuArgArgAspSerHis 180
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TITLE        Fetal Pituitary ESTs
JOURNAL      Unpublished (2003)
COMMENT      Contact: Zeguang Han
             Chinese National Human Genome Center at Shanghai
             351 Guo Shoujing Road, Zhangjiang Hi-Tech Park, Pudong, Shanghai
             201203, P. R. China
             Tel: 86-21-50801919(ex.45)
             Fax: 86-21-50801922
             Email: hanzg@chgc.sh.cn.
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                        GenCore version 5.1.6
            Copyright (c) 1993 - 2004 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on:     September 13, 2004, 19:20:35 ; Search time 80 Seconds
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Perfect score: 199
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Word size:  1

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4	124	62.3	771	3	US-08-985-526-28	Sequence 28, Appli
5	19	9.5	600	3	US-08-737-248-1	Sequence 1, Appli
6	19	9.5	1281	3	US-08-737-248-3	Sequence 3, Appli
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41	c	733	3.5	7	4	US-09-327-983-11	Sequence 11, Appl
42	c	749	3.5	7	4	US-09-833-381-1999	Sequence 1999, Ap
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                                ALIGNMENTS

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; Sequence 1416, Application US/09016434
; Patent No. 6500938
; GENERAL INFORMATION:
;  APPLICANT: Janice Au-Young
;  APPLICANT: Jeffrey J. Seilhamer
;  TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF SIGNALING
;  TITLE OF INVENTION: PATHWAY GENE EXPRESSION
;  NUMBER OF SEQUENCES: 1490
;  CORRESPONDENCE ADDRESS:
;  ADDRESSEE: INCYTE PHARMACEUTICALS, INC.
;  STREET: 3174 PORTER DRIVE
;  CITY: PALO ALTO
;  STATE: CALIFORNIA
;  COUNTRY: USA
;  ZIP: 94304
;  COMPUTER READABLE FORM:
;  MEDIUM TYPE: Floppy disk
;  COMPUTER: IBM PC compatible
;  OPERATING SYSTEM: PC-DOS/MS-DOS
;  SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
;  CURRENT APPLICATION DATA:
;  APPLICATION NUMBER: US/09/016,434
;  FILING DATE: HEREWITH
;  CLASSIFICATION:
;  PRIOR APPLICATION DATA:
;  APPLICATION NUMBER:
;  FILING DATE:
;  CLASSIFICATION:
;  ATTORNEY/AGENT INFORMATION:
;  NAME: Zeller, Karen J.
;  REGISTRATION NUMBER:    37,071
;  REFERENCE/DOCKET NUMBER: PA-0002 US
;  TELECOMMUNICATION INFORMATION:
;  TELEPHONE: (650) 855-0555
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;   TELEFAX: (650) 845-4166
; INFORMATION FOR SEQ ID NO: 1416:
;   SEQUENCE CHARACTERISTICS:
;   LENGTH: 970 base pairs
;   TYPE: nucleic acid
;   STRANDEDNESS: single
;   TOPOLOGY: linear
;   IMMEDIATE SOURCE:
;   LIBRARY: GENBANK
;   CLONE: g531102
US-09-016-434-1416

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; Patent No. 5585099
; GENERAL INFORMATION:
; APPLICANT: Richards, Sue
; APPLICANT: Kaplan, Joanne
; APPLICANT: Moscicki, Richard
; TITLE OF INVENTION: PROLACTIN AS ADJUVANT
; NUMBER OF SEQUENCES: 2
; CORRESPONDENCE ADDRESS:

;   ADDRESSEE: Brad Salcedo
;   STREET: One Kendall Square
;   CITY: Cambridge
;   STATE: MA
;   COUNTRY: U.S.A.
;   ZIP: 02139
; COMPUTER READABLE FORM:
;   MEDIUM TYPE: Floppy disk
;   COMPUTER: IBM PC compatible
;   OPERATING SYSTEM: PC-DOS/MS-DOS
;   SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
;   APPLICATION NUMBER: US/08/196,350
;   FILING DATE:
;   CLASSIFICATION: 424
; ATTORNEY/AGENT INFORMATION:
;   NAME: Gosz, William G
;   REGISTRATION NUMBER: 27,787
;   REFERENCE/DOCKET NUMBER: GEN 4-1.0
; TELECOMMUNICATION INFORMATION:
;   TELEPHONE: 6172527868
;   TELEFAX: 6173747225
; INFORMATION FOR SEQ ID NO: 2:
;   SEQUENCE CHARACTERISTICS:
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;   TYPE: nucleic acid
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;   TOPOLOGY: linear
;   MOLECULE TYPE: cDNA
US-08-196-350-2

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GenCore version 5.1.6
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Run on: September 13, 2004, 20:46:50 ; Search time 494 Seconds
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Searched: 304383 seqs, 251761380 residues

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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match *	Length	DB	ID	Description
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2	199	100.0	833	15	US-10-007-926A-93	Sequence 93, Appl
3	199	100.0	970	16	US-10-305-720-1416	Sequence 1416, Ap
4	199	100.0	1062	13	US-10-221-278-38	Sequence 38, Appl
5	199	100.0	1062	16	US-10-291-172-38	Sequence 38, Appl
6	199	100.0	1097	15	US-10-119-428-41	Sequence 41, Appl
7	178	89.4	832	13	US-09-065-330D-1	Sequence 1, Appli
8	177	88.9	603	10	US-09-819-094-1	Sequence 1, Appli
9	177	88.9	603	17	US-10-714-067-1	Sequence 1, Appli
10	128	64.3	603	17	US-10-449-609-2	Sequence 2, Appli
11	128	64.3	684	15	US-10-140-293-2	Sequence 2, Appli
12	128	64.3	1158	17	US-10-449-609-5	Sequence 5, Appli
13	124	62.3	390	14	US-10-036-869-26	Sequence 26, Appl
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15	81	40.7	423	10	US-09-819-094-3	Sequence 3, Appli
16	81	40.7	423	17	US-10-714-067-3	Sequence 3, Appli
17	81	40.7	603	10	US-09-819-094-4	Sequence 4, Appli
18	81	40.7	603	17	US-10-714-067-4	Sequence 4, Appli
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23 c	13	6.5	48	15	US-10-153-207-18	Sequence 18, Appl
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25	12	6.0	47	15	US-10-153-207-17	Sequence 17, Appl
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37	12	6.0	368	9	US-09-960-352-3831	Sequence 3831, Ap
38	12	6.0	368	9	US-09-960-352-6248	Sequence 6248, Ap
39	12	6.0	374	9	US-09-960-352-1938	Sequence 1938, Ap
40	12	6.0	378	9	US-09-960-352-4347	Sequence 4347, Ap
41	12	6.0	393	9	US-09-960-352-11400	Sequence 11400, A
42	12	6.0	398	9	US-09-960-352-9300	Sequence 9300, Ap
43	12	6.0	398	9	US-09-960-352-14259	Sequence 14259, A
44	12	6.0	407	9	US-09-960-352-5789	Sequence 5789, Ap
45	12	6.0	410	9	US-09-960-352-778	Sequence 778, App

ALIGNMENTS

RESULT 1
US-10-140-293-1
; Sequence 1, Application US/10140293
; Publication No. US2003022833A1
; GENERAL INFORMATION:
; APPLICANT: CHEN, WEN Y.
; APPLICANT: WAGNER, THOMAS E.
; TITLE OF INVENTION: USE OF ANTI-PROLACTIN AGENTS TO TREAT PORLIFERATIVE
; TITLE OF INVENTION: CONDITIONS
; FILE REFERENCE: 035879/0109
; CURRENT APPLICATION NUMBER: US/10/140,293
; CURRENT FILING DATE: 2002-05-08
; PRIOR APPLICATION NUMBER: US/09/246,041
; PRIOR FILING DATE: 1999-02-05
; NUMBER OF SEQ ID NOS: 42
; SEQ ID NO 1
; LENGTH: 684
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-140-293-1

Alignment Scores:

Left column

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Pred. No.:              4.06e-202        Length:        684
Score:                  199.00           Matches:       199
Percent Similarity:     100.00%          Conservative:  0
Best Local Similarity:  100.00%          Mismatches:    0
Query Match:            100.00%          Indels:        0
DB:                     15               Gaps:          0
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US-10-735-594-1 (1-199) x US-10-140-293-1 (1-684)

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Qy    1  LeuProIleCysProGlyGlyValAlaAlaArgCysGlnValThrLeuArgAspLeuPheAsp   20
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   85  TTGCCCATCTGTCCCGGCGGGGTGCCCGATGCCCAGTGACCCTTCGAGACCTGTTTGAC      144

Qy   21  ArgAlaValAlaLeuSerHisTyrIleHisAsnLeuSerSerGluMetPheSerGluPhe      40
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  145  CGCGCCGTCGTTCCACTACATCCATAACCTCTCCTCAGAAATGTTCAGCGAATTC          204

Qy   41  AspLysArgTyrThrHisGlyArgGlyPheIleThrLysAlaIleAsnSerCysHisThr      60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  205  GATAAACGGTATACCCATGGCCGGGGGTTCATTACCAAGGCCATCAACAGCTGCCACACT     264

Qy   61  SerSerLeuAlaThrProGluAspLysGlyGlnAlaGlnGlnMetAsnGlnLysAspPhe      80
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  265  TCTTCCCTGGCCACCCCCGAAGACAAGGGACAAGCCCAACAGATGAATCAAAAAGACTTT     324

Qy   81  LeuSerLeuIleValSerIleLeuArgSerTrpAsnGluProLeuTyrHisLeuValThr     100
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  325  CTGAGCCTGATAGTCAGCATATTGCGATCCTGGAATGAGCCTCTGTATCATCTGGTCACG     384

Qy  101  GluValArgGlyMetGlnGluAlaIleProGluAlaIleLeuSerLysAlaValGluIleGlu  120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  385  GAAGTACGTGGTATGCAAGAAGCCCGAGCCTATCCTATCCAAAGCTGTAGAGATTGAG      444

Qy  121  GluGlnThrLysArgLeuLeuGluGlyMetGluLeuIleValSerGlnValHisProGlu    140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  445  GAGCAAACCAAACGGCTTCTAGAGGGCATGGAGCTGATAGTCAGCCAGGTTCATCCTGAA    504

Qy  141  ThrLysGluAsnGluIleTyrProValTrpSerGlyLeuProSerLeuGlnMetAlaAsp    160
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  505  ACCAAAGAAAATGAGATCTACCCTGTCTGGTCGGGACTTCCATCCCTGCAGATGGCTGAT    564

Qy  161  GluGluSerArgLeuSerArgAlaTyrTyrAsnLeuLeuHisCysLeuArgArgAspSerHis  180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  565  GAAGAGTCTCGCCTTTCTGCTTATTATAACCTGCTCCACTGCCTACGCAGGGATTCACAT    624

Qy  181  LysIleAspAsnTyrLeuLysLeuLeuLysCysArgIleIleHisAsnAsnAsnCys       199
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  625  AAAATCGACAATTATCTCAAGCTCCTGAAGTGCCGAATCATCCACAACAACAACTGC       681
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Right column

```
; FEATURE:
; OTHER INFORMATION: prolactin (PRL) gene.
US-10-007-926A-93

Alignment Scores:
Pred. No.:              4.91e-202        Length:        833
Score:                  199.00           Matches:       199
Percent Similarity:     100.00%          Conservative:  0
Best Local Similarity:  100.00%          Mismatches:    0
Query Match:            100.00%          Indels:        0
DB:                     15               Gaps:          0
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US-10-735-594-1 (1-199) x US-10-007-926A-93 (1-833)

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Qy    1  LeuProIleCysProGlyGlyValAlaAlaArgCysGlnValThrLeuArgAspLeuPheAsp   20
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db   89  TTGCCCATCTGTCCCGGCGGGGTGCCCGATGCCCAGTGACCCTTGACCTGTTTGAC        148

Qy   21  ArgAlaValAlaLeuSerHisTyrIleHisAsnLeuSerSerGluMetPheSerGluPhe      40
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  149  CGCGCCGTCGTTCCACTACATCCATAACCTCTCCTCAGAAATGTTCAGCGAATTC          208

Qy   41  AspLysArgTyrThrHisGlyArgGlyPheIleThrLysAlaIleAsnSerCysHisThr      60
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  209  GATAAACGGTATACCCATGGCCGGGGGTTCATTACCAAGGCCATCAACAGCTGCCACACT     268

Qy   61  SerSerLeuAlaThrProGluAspLysGlyGlnAlaGlnGlnMetAsnGlnLysAspPhe      80
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  269  TCTTCCCTGGCCACCCCCGAAGACAAGGGACAAGCCCAACAGATGAATCAAAAAGACTTT     328

Qy   81  LeuSerLeuIleValSerIleLeuArgSerTrpAsnGluProLeuTyrHisLeuValThr     100
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  329  CTGAGCCTGATAGTCAGCATATTGCGATCCTGGAATGAGCCTCTGTATCATCTGGTCACG     388

Qy  101  GluValArgGlyMetGlnGluAlaIleProGluAlaIleLeuSerLysAlaValGluIleGlu  120
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  389  GAAGTACGTGGTATGCAAGAAGCCCGAGCCTATCCTATCCAAAGCTGTAGAGATTGAG      448

Qy  121  GluGlnThrLysArgLeuLeuGluGlyMetGluLeuIleValSerGlnValHisProGlu    140
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  449  GAGCAAACCAAACGGCTTCTAGAGGGCATGGAGCTGATAGTCAGCCAGGTTCATCCTGAA    508

Qy  141  ThrLysGluAsnGluIleTyrProValTrpSerGlyLeuProSerLeuGlnMetAlaAsp    160
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  509  ACCAAAGAAAATGAGATCTACCCTGTCTGGTCGGGACTTCCATCCCTGCAGATGGCTGAT    568

Qy  161  GluGluSerArgLeuSerArgAlaTyrTyrAsnLeuLeuHisCysLeuArgArgAspSerHis  180
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  569  GAAGAGTCTCGCCTTTCTGCTTATTATAACCTGCTCCACTGCCTACGCAGGGATTCACAT    628

Qy  181  LysIleAspAsnTyrLeuLysLeuLeuLysCysArgIleIleHisAsnAsnAsnCys       199
         |||||||||||||||||||||||||||||||||||||||||||||||||||||||||||||
Db  629  AAAATCGACAATTATCTCAAGCTCCTGAAGTGCCGAATCATCCACAACAACAACTGC       685
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